

FIGURE 1

ACTGCACCTCGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTGCCTTCCCCG
CAGCGCTACCGCGATGCGCTGCCGCGGGCGCCTGGGCTCCTGCCGCTTGTGCTG
CTGCTGCCGCCGCGCCGGAGGCCAAGAACGCCACGGCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTAACCAAGGGGATGGTGGACACCGAAAGAACGAGATTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGGCCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAAGGGGAATGGCACTGCAGCGAGATGGGAGCAGACA
GGGGCAGGGCTCTGCCGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCCGCTGTGATGTGGACGGAGTGTGCGGCCAGGCCCTCCCTGCAGCGCTG
CCGAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGACGAGTGTCACTAGCAGAAAAAACCTGTGAGGAAAAACG
AAAACGTCAAAATACTCCAGGGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCCTGTGCGCCGCGAGGGCTGAAGGCCACAGAACGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGACTTACCCCTTAAATTATTCAAGAGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCTGCAGTGGACAGCGGGGGAGGGCTG
CTGCTCTCAACGGTGATTCTCATTTGCCCTTAAACAGCTGCATTCTTGGTTCTTCTT
AACAGACTGTATATTTGATAACAGTTCTTGTAAATAAAATTGACCATTTGAGGTAATCAGG
AGGAAAAAAAAAAAAAAAGGGCGCCGCACTCTAGACTCGACCTGCAAGC
TTGGCCGCGCATGGCCAACCTGTGTTATTGCAAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAAATTTCACAATAAACGATTCTTCACTGCATTCTAGTTGAGGTTGTCAAACACTC
ATCAATGTATCTTATCATGCTGGATCGGAATTAACTCGCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTAACCTCTGAGGCGGAAAGAACCCAGCTGGAATG
TGTGTCAGTTAGGCTGTGGAAAGTCCCGAGGCTCCCGAGCAGGAGCAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRAALGLPLLLLPPAPEAKKPTPCHRGRGLVDKFQNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCCESSDPECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLLKVCCSPGTYGPDCCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQQPLCTDCMDGYFSSLRNEHTSICTADESKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVPDPGEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTGACCACCGTCCGCCAGGCCGGAGGCAGCCGCCAGCGCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGGCCAGCAGAGTATCTGACGGCGCAGGTTGCCTAGGTGCG
GCACGAGGAGTTTCCGGCAGCGAGGAGGTCTGAGCAGCATGGCCGGAGGAGGCCCTC
CTGGCCGGCTGAGGAGGAGGAGGCTGACCTATGGATCGATGCTCACCAAGGAAGAGTACTCA
TAGGATTGAAGAAGATATCTGATTGTTTCAGAGGGAAAATGCCACCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTTATCTGTAATATCCATTGCAATTTCAG
CTGGCAAGCTGCAGGGCAGGAGAATACTCTATGAATTCTCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCATGCTCCCTGCTGGAACAGTGCCCTCACAGGCA
TCAGTTGTTCAAGTGGTTCCATGTCCTGGAAAAACAGGATGGGGGGCAGCATTTGAAGT
GGATGTGATTGTTATGAAAGGCAACACATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAAACAGCTGAGTGCCTCAGGGGGTGGCGAACATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGGTGCTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACAGATGTGATGAATGGGACTTTGTGTGACTCTGTTCTGCACTGCCACCTG
GATTCTATGGCAGTAACCTGACAAAGGAAACTGCTCACCCACTGCTTTAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTTATTGCCCCCAGGACTAGAGGGAGAGCAGTGTAAATCAG
CAAATGCCACAACCTGTCGAATGGAGGTAATGTCATTGGTAAAGCAATGTAAGTGT
CCTGGAGGTTACAGGGAGACCTCTGTTCAAGGCTGTCGAGGCCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACATGTCAGGAGGTGGCATGGAAGACACTGCAA
TAAAGGTAAGCAGGCCAGCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGAGC
ACACGCCCTCACTTTAAAGGCCAGGGAGGCCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGCACATGAAACGTTTAAGTACACCAAGTTACAGGCCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTATTACACTTAAGAATACTGGCCCTGAATTTTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCCTGAG
CATGATGGTATAGATTTCCTGTTCACTGCTTTGGGACAGATTATATTATGTCATTGTA
TCAGGTTAAAATTTCAGTGTGAGTGGCAGATATTTCAGGAAATTACATGCAATTATGGT
GTCTGGGGGAGGGAAACATCAGAAAGTTAAATTGGGCAAAATGCCAGTCAAGTCACAGAAT
TTGGATGGTCACTGTTAAATGTTGAAGGTTACAGCATTTCAGGTTATTGTCAGATATTAGAT
GTTGTTGTTACATTAAAATTTGCTTAAATTAAACTCTCAATAACAAATATATTGGACC
TTACCAATTTCAGAGATTCACTGTTAGTAAACACTGTTGAGTGGCATTT
AAACAAATATAATATATTCTAAACACAATGAAATAGGGATAATAATGTAACATTGGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAAAACATTGTTAT
ACTGTTTGTATGTTAAATAAAGGTGCTGCTTTAGTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTGGC
CCCATGGCCAACTTGTATTGAGCTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDTVIMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCUTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSCKCSKGYQGDLCSPKVC
EPGCGAHTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCGGCGGAGAGCCAGGAGGCCAGGGCGCGGGCCAGCTGGG
CCCCAGCCCCAACCTTCACCAAGGGCCCAGAGGCCACCATGTGGCATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGCTGTCGGCGCCGG
GAGCTAGCACCGGGCTGCACTCGGGGATCTGGGGACGGGAGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGGCGCTCCGAGCACTGTGCTGGCTACCTGGGGCCCATCT
GTTACTGTGACCTCTCTGCAACCGCAAGGCTCCGACTGCTGCCCTGACTCTGGGACTTC
TGCCTCGCGGTGCCACCCCTTTTCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGGAACGTACTGGACAACGTAAACGGTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCACAGATCAAAAGCCATCAACCCAGGCAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCTGGATGAGGGCATTGCTACCGCTGGGACCCA
TCCGCCCCATCTCCCTGGTCATGAACATGCACTGAAATTTACAGTGTGTAACCCAGGGAG
GTGCTTCCCACAGCTCGAGGCTCTGAGAATGGCCCAACCTGATTCTCATGAGCCCTTCTGA
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCCACAGCAGCTGTCATCCGATCGTGTCT
CAATCCATTCTCTGGACACATGACGCCCTGTCTGTGCCCCAGAACCTGCTGTCTGTGAC
ACCCACAGCAGCAGGGCTGCCGGTCTGATGGTGCCTGGTGGTTCTGTGCTGG
CCGAGGGTGGTGTCTGACACTGCACTACCCCTTCCTGGGGCTGAAAGACAGGAGCTGGCC
CTGCGCCCCCTGTATGATGCACAGGCCAGGCATGGTCTGGGCAAGCGCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAAATAACATGACATCTACCAAGGTCACTCCGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACATGGCCCTGTCCAAGGCCCTCA
TGGAGGTGCATGAGGACTCTTCTCTACAAAGGGAGGATCATCAGGCCACAGGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGAGCCTCAAAATACTGGACTGCGCCAACTCTGGGGCC
CAGCCCTGGGGGAGAGGGGCAACTTCCGATCGCGCCGCTCAATGAGTGCAGACATCGAG
AGCTTGTGCTGGCGCTGGGGCCGCTGGGAGGATCATGGGTCTACTGAGGCTG
CGGGCACCACCCGGGGTCCGGCTGGGATCTCAGGCTAAAGGGCCGGCGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCCCGCAGAGGCCGGGCGCAGGCCGGGCGCAGGCCGAGACTGGCG
CCGGCCGGGTTCCGCTGACGCGAGGCCGGCGCTGGGAGGCCGGGCGCAGGCCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGAGCCGGCAGGGCTGGGAGAGGACACAGCTGCAG
ATCCCAGGGCTCTGGCGCCCCACTCAAGACTACAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTAGACAGGGTCTTGTCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCCATCAGGCTCACTGTAACCTCCGACTCTGGGTTCA
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTTGATTTTTGTAAGAGGGGGCTCACTGTTGCCCCAGGTGGTTTCGAACCT
CCTGGGCTCAAGCGGTCAACTGCCCTCCCAAAGTGTCTGGGATTGAGGCC
ACTGACCCAGCCCTGATTCTTATTCTCAGATATTATTTCTTTCACTGTTAAAAA
TAAAACAAAGTATTGATAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYCQEQLLCRGRADD
ALPYLGAICYCSDLFCNRTVSDDCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTGGGACACATNACGCCCTGTCCTTNGCCCCAGAACCTGCTGCTTGTACACCCAC
CAGCAGCAGGGCTGCCCGCGNTGGCGTCTCGATGGTGCGCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGGGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCACAGGAGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGG
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAC TGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCCGCTGCTCCCTGCACTCGGCCCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCCACACTGGGTGTGGTGCCTCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCACTGGGAGCCTGTCCTGGTTCTGAGGCACATCTTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGGCCCTCTCCAGGACTCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCTGCAGATGGCCCTCCAACCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCTCTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTCCTGGAGTCTCCAGAGATGGGCCCTGGAGGGCTGGAGGAA
GGGGCCAGGCCACATTCTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHR^{TTT}WARRTSRAVTPCATPAGPMPCSRLPPSLRCSLHSACCSDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWE^PVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQI^{SS}SDT
DPPADGPSNPLCCCFHGP^AFSTLN^PVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRR^AQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCTCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGGCGCAGATCCGCAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGGACGGACACGTTGGCAGCCGGGTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAAGCCCAGCGGGAAAGCAAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACCGCCAGGGGCCCGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCAGGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAACGAGAACAGCTCGAGTTGTGGCTCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCAAGCCCCTCACGTAGTCTGGAGGCAGGGCAGCACCCCTGGGCCCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCCGAAGCATCGAGCCCCCAGCTGGGAAGGGGCAGGCCGTG
CCCCAGGGCCGCTGGCACAGTGCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGACTGAAGGCCCTGAGACAAACCGTCTGGAGGTGGCTGTCTCAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCAGGCCCTGCACCCACCCCAACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDGVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGAAAGAGGGCAACACAGGCTGATAAGACCAAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTCTGGACTTCAACAGAACCCCACAGT
CATTTTGATTTGCTTTTATTTTCTTTCTTTCCACACATTGTATTTAT
TCCTGACTTCAAGAAATGGCCCTACAGACACAAAGATGGCCAGGCCATGGGCCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTC
CAAACCTCTGGCTGCCAGAGAATTGTACTCTACCTCCACAAACAACCAAAATTAAATATGC
CTAGTGTGTGCCGCTGCGACAGGAATTGTACTGTAAATGAGCGAAGCTTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACGGTACTCTACCTCCACAAACAACCAAAATTAAATATGC
TGGATTTCCTGCGAGAACTGCACAACTGTACAGTCGGTGCACAGGTCTACCTGTATGGCAACC
AACTGGACGAACTCCCATGAACACCTCCCAAGAATGTCAAGATTCTCATTTCAGGAAACAC
AATATTCAAGACATTTCACGGGCTGCTTGCCCAGCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCATCCACAGTGGGGGTTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAAATTGTTGTTTGTCTAAAGATCACCCTGAGCTGTTGCTGTGATATCCGACATGGCCTTCCAGAA
TTGCAAGAGCTGAGAGTGGATGAAAATGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCAGCAGCTGGAGGCTCTTATGTCAGGAAACCTCTGACCAACAAAGGGTATGCCG
AGGGCACCTTCAGGCCATCTCAACAGCTCAAGGAATTTCAGTAATTGCTGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCGAGAT
AAACACACATTCTTGTACAGCCTCTCAATCTGCTGAAGCTGGAAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTTGATAATCTCCACACTGAAAGCAGCTC
ACTGCTCGAAATAACCCCTGGTTTGTACTGAGCTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTCATCTCTCAACGTGCGGGTTTCATGTCAGGCAAGGTCTGAAACACTCGGG
GGATGGCGCTCAGGAATTAAATATGAATTCTTGTCTGTCCCACAGGACCCCCGGCCTG
CCTCTCTTCCACCCAGGCCAAGTCAGCCTCTCCGACACTCAGCCTCCACCCCTCTCTAT
TCCAAACCCCTAGCAGAAGCTACAGCCTCCAACTCTCACCCACATGAAACTTCCCAAGGATT
CTGACTGGGATGGCAGAGAAGAGTGCACCCACCTATTCTGAACGGATCCAGCTCTCTATC
ATTGGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTTCACCGTGATGGCATA
CAAACTCATGGGTAAGGGCCACAGTTAGTGGGGCATCTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACTGAGCCTGGTTACTTAGAGCCCGATCCACCTATCGGATT
TGTGTTAGTGCCTACTGGATGCTTTAACTACCCGGCGGTAGAAGACACCATTTGTTGAGAGC
CACCACCCATGGCTCTTATCTGAAACAGCGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGTCGGCGGGCTTGTATGGGGCGCGGTGATATT
GTGCTGGTGTCTTGTCTCAGCGTCTTTGCTGGCATATGCACAAAAAGGGCGCTACACCTC
CGAGAAGTGGAAATACAACCGGGGGGGGGGGAAAGATGATTATTGCGAGGGCAGCCACAAAGA
AGGACAACTCCATCTGGAGATGACAGAAACAGCTTCAAGATCGTCTCTTAAATAACGAT
CAACTCTTAAAGGAGATTTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTCCAGACCTGGAGC
ACTGCCATACGTGAAGCCAGAGGGCCAGGGTTATCAAGGGGAAACATTAGACTTGGAGAA
CACACTCGTGTGTCACATAAGACACGCGAGATTACATTGATAATGGGATTAAAAAAAGTG
CTATTTCTATTCAAGTAAACACAGTTGTAACTCTTTGCTTAAATCTTGTAACTCTTGTAAATCTT

FIGURE 13

MGLQTTKWPSPHGAFFLKS^WLIIISLG^LY^SQVS^KLLACPSVCRCDRNFVVCNERSLT^SVPLG^IP
EGTV^VLYLHN^NQINNAGFP^AE^LHNVQSV^HT^VLYGNQLDEFPMNL^PKNVRVLH^LQENNIQ^TI
SRAALAQLLK^EELHLD^DDN^SI^TVGVEDGAF^RE^AISL^KLLFLSK^NHLSVPV^GLPV^DLQ^ELR
VDENRIAVI^SDMAFQNL^TSLER^LIVDGN^NLLTNKGIAEGTFS^HLTKL^EFS^IVRNSL^SH^{PP}PD
LPGT^HL^IR^LY^LQDNQINH^IPLTAF^SN^LR^KL^ERL^DISNNQ^LRMLTQGV^FDN^LSN^LK^QL^TAR^{NN}
PWFCD^CS^IKWVTEWLKY^IP^SLN^VR^GF^MC^QG^PE^QV^RGM^AV^RE^LN^MN^LLSCPT^TTPG^LPLFTP
APSTASPTTQPPTLS^IP^NP^SR^SY^TP^PT^ITS^KL^PT^IPDWDGR^RVT^PP^IS^ER^IQL^SIHFVN^D
TSIQV^SW^LSLFTV^MAY^KL^TW^VKM^GH^SL^VG^GI^VQ^RE^IV^SG^EK^OH^LS^LV^NL^EP^RS^TY^RI^CL^VP^L
DAFNYRAVE^DTIC^CSEATTHASY^LNNGSNTASSHE^QTTS^HSM^GP^FL^LAGLIGGA^VIF^VL^VL
LSVFCW^HM^HK^GR^YT^SQ^KW^YN^RG^RR^KD^DY^CEAGT^KKD^NS^ILEM^TE^SF^QI^VS^LNN^DQ^LK^G
DFRLQPIY^TPNGGINYTDCH^IPIP^{NN}MRYCNSSVPD^LE^HC^HT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACCTGGGCAAGCGCGCGCGGGAGACAGGGCAGAGGCAGAGGTGGGCTCCGCTCTCGCTCCACAGAGCG
ATCCCCGAGAGAGACCCGGCGCTCGGGAGGGAGAGGGCAGAGGAAGACCGGGTGGCTGCCCGCTGCC
TGCGCTCCAGGAGCATGGGAGCTGGCGCTCGAGCCCTGCCCTCTGCTCGCTGCCCTTGAAAGAATGGCTCGAGGT
GCTTTCTGAGATCTCGGGAGCATGGGCTCTGCCCTGCCCTGGCGAGGGAGGGCTCACGTGGGAGGTCCATCT
CTAGGGGAGACACGCTCGGGAGACCCACCGCAGACGGGCCCTCTGGAGAGTTCTGTGAGAACAGCGGGAGAC
TGGTTTCTCATCATGACAGCTCTGGAGGTGGCGAGGGCTGCTGAGAGGTGGGAGCTGGCTCACGTGGGACA
TCTGCAATTCTGAGATCTGGCTCATGTCACCGAGTGGGCTGCTCCAATAATGGCAGCACTGTCAAGAAATG
AGTCTCTCCCTCAAGACCTTCAGGGAGGTGGCGAGGGCTGCTGAGAGGTGGGAGCTGGCTCACAGCG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAGACATCGCAITCTGAGAGCAGAGGGGCCCGGCCCCCTGA
GGGAGAAATGTGCCAGGGTCATAATGATCTGAGACAGATGGGAGACCTCAGGGACTCTGGCCAGGGTGGCTGA
AGGCACGGGACACGGGACATCTAATCTTGGCCATGGTGGCCAGGTGACTCTCAACACCTTGAAGTCCATG
GGAGTGAGGCCCATGAGGAGCATCTTCCCTGTGGCCAAATTCTGAGGAGATGTGAGCGTGAACCTGGCT
AGAAGAAGGTGGCCAGGAGCATGTCAGGAGGATCTCTGGCCACTCTGAGACATGGTGGGAGCT
GCTCATCGTCTGGAGGAGGAAACAGGCTAACATCTGGAGCAGGACTCTGGAGGAGCTTGCAAGATCCAGTGT
GTGCCATGGAGGCCAACAGGACTGTGAGCAGCAGCTCTGGTAATGTGCGGGCTCTCTGCTGCGAGTGTCAAGCTG
GCTACAGGCTCTGGAGGAGGTGGCTGAGGAGCTGCTGAGGAGCTACTGTCCTCAGAAAACACCAGGATGTGAC
ATGAGTGTAAATGCTGATGCCCTACCTTCTGGGAGCTGCCATGAAGGAGTTGCTCTAACCCAGATGAAAAAA
CTGGCAAGAGTAACAGCTGCACTGGCAGGAGGAAACCCGGCTGTGAGCATGAGTGGCTAACATGGAGAGGACT
ACTACTGGGCTGCCACGGCTGGCAACTCTGGCAACCCATGGCAACGGGAGCTGGGACACTCTGGCAG
AGCAGGAGCATGGCTGTGAGCAGCTGTGAGACACGGAGGATCTCTGGCTCTGAGCTGGCTAACAGGCTTCC
TCATCACTGGAG
GTGTCACATGGACAGATCTTCTGGCTGTGAGCTTCTGGAGGAGCAGCTGGCTCCGAGGGATGGAAAGACGTG
CAAAAGTGTGAGGTTATATACTCTGGTAAGAATGGAAAACCTCTGAGAAGGAAAGATGTCCTGCAAGCTATAG
ACCATGTCCTGTGAGACATTTGTGAGAACAGTGAACACTCATACAGCTGAGGTGGAGGAGGATTCGGCTCG
CTGGAGGATGGGAAACCTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
ATATAATGGGAAATTCTACATCTGCAAAATGCTCAGAGGATTCTGTTCTGAGGAGCTGGGAAACACATTGTGTTA
GCACTGAAGGGCAATTGACCTGCTCTGGCTCTGGTGTGAGTGTGAGTGTGAGGAAAGAGAAATTGGAGGTG
TGAGGAGCTTGTGACTGGAAATTATGATTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
ACATCCACACAGGCTCACACAGACTCTACTCTGAGGAAACCTTCACACTGAGGAGGAGGAGGAGGAGGAG
ACATGAAATACTGGGAAAGGGCTCTGACTGCTGGGCTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG
GAGAAGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
ACGCTCTGGAGTGGGGCCAGTAAAGGCAAGGGCAATGGTATCACTATGTTGAGCTGTGTTGGGTAGGAAAAGGCCATTG
AGGGAGGAACTCAAGAGATGTGCTCTGAGCCCACAAACAGGACATCTCTGAGGAGCTGGAGGAGGAGGAG
ATGAGATAAGTGAACAAAACCTCAAGAGAAAGGAGCTGTGAGGAGCTGAGGAGGAGGAGGAGGAGGAG
CAGGGGAACTGCCAACAGGCTCAAGGCCAACAGGCAACAGGAGCTGAGGAGGAGGAGGAGGAGGAG
CTCTGTTCTAATTCTGAGTGTGCAACAGAGATATCTGTTGAGAAGACAGACATCTTCTGGCTCTACACAAAAGCTT
CCCAATTCAACAAAACCTTCAAGGGAGGCCCTTGGAGGAAAACACGATCAATGCAAACTGTAATGGAAAACCTTATAATGT
TCCAGAACCTGGCAACAGGAGAAGTAAGAAAATTACACAGGCTTGAAGAAAATGACACAGAGATGGAGAGGCC
TGGAAAATGCGCTGAGATACAGATGAGAATGAGAAAATGGGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGGAGTGCAGAGGCCCAAAAGCTCAGGGTATTGTTAAATCAATGTTGAGGTAAGGTAAGGAAACAAATCAGTACTGA
GAAACCTGGTTGCCAGAGAACAAAGACAAGAAGATATACTAACAATCTGTTGAGGAGGAGGAGGAGGAG
TCAGAATTCTAAGATGAAATTACACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGAGAC
AACTGCTCTGCCCTCATCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCAAGCTTACT
CTGAGAACACTGGCCATAGGAATGTGTTTTGTACTGGAGCTTACCTGTATATGATATGATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAGATTTTATAACATATTAAAATCACCACITCAG

FIGURE 15

MEKMLAGCFLILGQIVLPAEARERSRGRSISRGRRHARTHQPQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGDVTRVGLLQYGSTVKNEPSLKTFRKSEVERAV
KMRMRHLSTGTMGLAIQYALNIAFSEAE GARPLR ENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI GVGQVDFNFTLKSIGSEPHEDHVFVLANFSQIETLTSVFQKKLC TAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVADVDYCASENHGCEHECVNADGSYLCQC HEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCRSDVYCLLS DHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDS CALGDHGCE
HSCVSSSED SFVCQCPEGYLRLREDGKTCRKDVCQAIDHGCEHICVNNSDSYTCECLEGFRLA
EDGKRCR RDKVCKSTHHGCEHICVNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGII DSLTISPKAARVGLLQYSTQVHTBFTLRNFNSAKDMKKAVA
HMKYMGKGSMTG LALKHMFRSFTQGEGAPRLSTRVPRRAIVFTDGRAQDDVSEWASAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHIFYAEADFSTMDEISEKLKKGICCAELEDSDGRQDS
PAGELPKTVQQPTESEPVTINI QDLLSCNSFAVQHRYLFEEDNLLRSTQKLSHSTKPGSPL
EKHDQCKCENLIMFQNLANEVEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCGGCTGGCAGGGAGGGC
CATGATTCCCCTCCGGGGCCCTGGTGACCAACTTGTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCCAACGGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCCTCCAGCGTGGTACACCTTGACGGGAGGTGCTTC
ATCCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTCATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGCCCCGCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTAATGGTCCAGCTCCATCTGGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAAACGTGACCCCTGAGCTGCCAGTCTCAAGGAGTAAGCCCGTGTCCAATACCA
GTGGGATCGGCAGCTCCATCTTCAGACTTCTTGCACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGGCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCAGCAAGGCCAC
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAGTGGACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGGTACCTGGTTGGACTGGGGTGTGGCTGGCTGGCTGGTCC
TCTTGTACCACCGCGGGGAAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCCCT
TTCCCTGTCACTCCGCACGCCCTCCGGCACCCCATGGCCCTCCAGGGCTGGTGCAT
TGACCCCCACGCCAGCTCTCCAGCCAGGCCCTGCCCTCAGCAAGACTGCCACGACAGAT
GGGGCCACCTCAACCAATATCCCCATCCCTGGTGGGGTTCTCTCTGGCTTGAGCCG
CATGGGTGCTGCTGCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GAC**
CCACCAACTATTGGTAAAGGATTGGGGTCTCTCTTCTATAAGGGTACCTCTAGCAC
AGAGGCCCTGAGTCATGGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCCCAACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTTATGAAGGCCAGCTG
CTGAAATTAGCTACTCAGCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCTCCAGGC
CCCTTGATCTGACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAACATGAAATATGTGTTGGTTCTGGCAAATTAAAGATACTAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACNCVTLLEVSTGPAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPSLSSQALPSRPLPTTDGAHPQPISPPIPGGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGGGCCACGCCAATGAAACGCCCTCCGCTCTAGTGGTTTTCCACTTGTG
TTGAATTGTTCTATACTCAAATTGACCAAGCACCTGCTCCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAACGCCCTGCTATTGACACATGGGATTTCAGGAAATGGTGCACAA
TTTGAGATGATAATGAAATGGGAAATTAACTCAGTCTGTTGGCGAAATGCTAATTGCA
ACTAACACAGAAGGAAGTTATTATGATGTTGTAACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGGAACGCCCTGCTATAGAAAATGTGAATGCAAACCTGCCATT
TAGATAATGCTGTATAGCTGCAAATATTAAATAAAACTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTACAGAAGTCTAGAGAAAATCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTACTGTAATCATCTCATTACTAGGTTACAGAACACA
CTATCTCAGCCAAGGACACCCCCCTACACTCAACTCTTACTGAATTGAAAAACCGTGAAT
AATTGTTCAAAGGGATACTTGTAGTTGGGACAAGTTATCTGTAATCATAGGAGAAC
ACATCTACAAAACCTCATGACACTGGTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACACAGAGTTGATCAAATTCAGGATATACTCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAGAGAGAAAGCTGATGATGAACTGGCAATGTTGCAAGTGCATTTTATATTATA
AGAGTATTGGTCTTGTCTCATCTGACAACCTTATTGAAAACCTCAAAATTATGAT
AATTCTGAAGGGAGGAAAGACTCATCTTCTGAGTAACTTCTGATGCTCAATGAGCTCAAACCC
ACCCACATTATGAACTTGAAGGAAATAACATTACATTAAGTCTGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCTTTGGAAATTACTCACCTGATACCCATGAATGGCTGGTCT
TCAGAGGGCTGTGAGCTACACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCT
GACACATTTCGAATTGATGTCCTGTGCTTGTGATTAAAGATTATAATTCT
TTCAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCAATT
ACCTCTGGTCTTCAGTGAACATTCAAAGCACCGAGAACAACTTCAAAATTCTTGCTG
PGCCTATTCTTCTGCTGAACCTTGTGTTCTGTGGATCAATCAAACAAACTAATAGCT
TCTGTTCAATCATTGCGGACTGCTACACTACTCTTTAGTGTGTTGATGGATGTG
ATTGAAGGCATACATCTCATCTCATCTGTTGCTGATGATGTTGCA
CAAAGATTATATCTTGGCTATCTAGGACCAACGGGCTGGTAGTTGGGATTTTGGCAGCAC
TAGGATACAGATATTATGGCACACCAAAGTATGTTGGCTAGCACGGAAAACAACCTTATT
TGGAGTTTATAGGACAGCATGCTTAATCATTCTTGTGTTAATCTTGGCTTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCGGGTTGAACACAGAAGTTAGTTGCTTGGAAACA
TAAGGTCTTGTCAAGAGGGACCCCTGCTCTCTGTGCTTCTCGGCCACACCTGGATCTT
GGGTTCTCATGTTGTGCAAGCATGTTGCTACAGTGGTTACAGCTTACCTTACAGTCAGAACATGC
TTTCCAGGGGGATGTTCAATTCTTATTCTGTTGTTTATAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCTCTGTTTTGGATGTTTAAGGTAAACATAGAGAATG
GTGGATAATTCAACTGCACAAAATAAAATTCCAGCTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCTAAATTATTAACACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACCTGAGATAATAAGGTAATTGTTGATCATATAGATATACTATG
TTTCTATGAAATAGTCTGCAAATAGTATTGAGATATTGAGATATTGAAAGTAATTGTTT
CTCAGGAGTGAATCATGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATGAA
TGTCTGAAAGGAAACCACTGGCTTGATATTCTGTGACTCTGTTGCTTGGAAACTAGTCC
CCTACACCTCGGTAACTGACCTCCATTACAGAAAGTGGACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAGGGAAATGATAAGATGTTGAACTGACTGTTTCTGTAGAC
TAGCTGAAAGAATTGTTGACAAAAAAGAATTGAAAGAAACATTTTACCTTGTGAA
TTGTTCTGAACTTAAATGTCCTAAACAAACTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATCTAAAAAAAAAAAGGTTACCTCCACAAATTGAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRPLLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENACTNTEGSYCCMCVPGRSSSNQDRFITNDGTVCIENVNANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEVRNSVTDLSPTDIITYIELAESSLLGYKNNTISAKDTL
NSTLTLTEFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTEQATLRISQSFKTTEFDT
NSTDIALKVFFFDSYNMKHIIHPHMNMMDGDIYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNHLLTHFAILMSSGPGSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAWMCIEGIGHLYLIVVGVLYNKGFLHKNFYIFGYLSPAVVGFSAALGYRYGGT
TKVCWLSTENNFIFSFIGPACLIILVNLLAFLGVIIYKVFRHTAGLKPEVSCFENIRS CARGA
LALLFLLGTTWFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCATCGAAAGGTCAACAGATAAGGTATA
ATTATATGAACTTGAAAAAAACATTACATTAAGTCATCGAAAGGTCAACAGATAAGGTATA
GGAGTCTATGTGGATTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGTGATGTCCTCTGGCTTCCATTGGTATTAAGATTATAATATTCTTACCAA
GGATCACTCAACTAGGAATAATTATTCACTGATTTGTCTTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTCGCGGGTGGGGAGGAGTTCCCGAAACCCGGCCG
CTAAGCGAGGCCCTCCTCCCGCAGATCGAACGCCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCCTGCCCTGCCCGGGCCGGGGAGGGGGCTGGGGCTGGGGCGGAGGCCG
GGTGTAGTGTTGGGGCTGGGGGGCGGGAGGCTTGTATGCAATCCGATAAGAAATGCTCGG
TGTCTGGGCACCTACCCGGGGCCCTGAAGCGCTACTATATAAGGCTGCCGGGCCGGAG
CCGCCGGCCCGTCAAGAGCAGGCCCTGCCCGAGCATCCCGCTGCCGCCAGCCTCCCGCACCCCATCGCCG
GGCACTCACAGCCCCGAGCGCATCCCGCTGCCGCCAGCCTCCCGCACCCCATCGCCG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGAGCGGGGTGTTGTTGACGGTACATGG
ATCCCTGGCCGGCCTCTGGCTGGCCCGGGCCGGCCCTCTCGGACGCCGG
CCACGTGCACTACGGCTGGGGCACCCCATCGCCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGGCTCTCAGCTGCTTCTCGCATTCCGTGCCGACGGCGTCGTGAACTGCGCGGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCACTGGCGCCGACGGCAAGATGCAAGGGCTGCTTCACT
ACTCGGAGGAAGACTGTGCTTCGAGGGAGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCCCTCCCGTCTCCGTAGCAGTCCAAAAGCGCGCAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCATTTCTGCCCATGTCGCCCATGGTCCCAGAGGAGCTG
AGGACCTCAGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGTCAAGGACTGGAGGCCGTGAGGAGTCCAGTTGAGAAGTAAC
GAGACCATGCCCTTCAACTGCTGCCAGGGCTGTGTTGACCTGCACTGGGGAGC
TGCTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAAAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGGAAATAGACTTGTCTGAT
CATAAACATTGTAAGCCCTGAGCTTGTGCCAGCTGCTGCTGGGCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGTTGAATACCTCCATCGATGGGAAC
TCACCTCTTGGAAAAAAATTCTTATGTCAGCTGAATTCAGTCAACGTTCTCATACCTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTAATTTCAGGAACAGGTGATCCACTCTGTA
AAACACGAGGTAAATTTCACCTCAACCCCATGTTGAATTTGATCTATATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCGATGGCCACCCAG
GCTTCAGGAGTAGGGGAACCTGGAGCCCCACTCAGCCCTGGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATACTTGTGCTGCCGGTGTACCTGC
TTCCATCTCCCAAGCCCCACCCAGGCCCTGCCAACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCCTACCTTATGTCACCTCTGTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCAAAGTCTTGTCAATAACTTGTGTTGAAAGCAGCGGGGGAGACCTAGAAC
CTTTCAGGCCAGCACTTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATGCCCCAAATTATATTATGTTGATGTAAGTGAAGGTTG
TTTGTATATAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEKAVALRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGGAAGATGCGAGGAGGAGCCGCCACGCCCTCCTGCTG
CTGCTGCGTACCTGGTGGTCGCCCTGGCTATCATAAAGGCCTATGGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCTTGTCTAC
TATCAACAGACTCTTCAGGTGATTITAAAAATCAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACCTGGAAGTATTAGTGGCTCCAGCAGT
CCATCATGTGAAGTACCCCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAAATCCAGCTCTGAATACACATGGTTAACGGATGGCATCCGTTGCTAGAAA
ATCCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAAATGAATACAAAAGTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT
TGTGGATATCGCAGGTGCTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTGTGGCTTAGTGATTTCCTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAATGTGCACTGGCTCACGCCCTGAATCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCACTCTGGCAATATGGTGAACACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGAGGGCGAGGTGAGCTGAGATCACG
CACTGCAGTCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TWTLEVLPAPVPSCEVPSSALSGTVVELRCQDKEGNPAPETYWFKD
GIRLLENPRLGSQST
NSSYTMTKTGTLQFNTVSKLDTGEYSCEARNNSVGYRRCPGKRMQVDDLNISGIIIAVVVA
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGGGGCTAGCACTGAAACTGCTTTCAAGCAGGAGAAGGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCTGGCAT
CATGCTGCTATTCTGCACAAACTGAAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAAATTACTCAATCTCTATGACCATCTACATACACTCCACCTCAAAGTACATCAATA
TTATATCATTAAAGGAAGAATAGTAAACCTTCTCTCTCAATATGCACTGGACATTTTGAGAACATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAACCTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTCCTTATCAATCAGCCTTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGGCCCATTACATTTCTGAAGAAGAAGCTAAGATGAAGGACATGCCACT
CGAACATTCTATGCTACTTGGCCTAGTCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTAGTGTGAATCAGGCTTGTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCACAGACTAACATATTGCAAAAAATTGAATCTCCACAG
ACTTTCCAGTAACCTTACTGGCCTGGATTATCCTAAACAACTTATCTCAGTCACCAAT
ATTAATGTAAAAAGAGTGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTACTGA
ACTGCTCTGAAAATGTCTGTGGCAACTGACCAACTTACAAGAACTTATAATCACAACT
TGCTTCTACAAATTCTACCTGGAGCTTTATTGGCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAAGTCAACAGTAAGTGGTTGATGCTCTCCAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
ACTTCCGCAGCTGGTTATAGCTGGTATAACCTCACGAAAATACCGAGATAACGCCCTGGTT
GGACTGGAAAATTAGAAGACATCTCTTACAGAACAGGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAGATTGTAATCTCAATTGGATCTAAATAAAATCTTATAATGAA
TACGAAGGGGTGATTAGCAATATGCTACACTTAAAGAGTGGGATAAAATAATGCT
GAGCTGATTCTCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACACCCCTAGATTGCTTACATTCCACCCAACTGCACTTTCAGACTCCCCAACGCTGG
AATCACTCATGCTGAACAGCAATGCTCTAGTGCCCTGTACCATGGTACCTGGAGTCTCTG
CCAAACCTCAAGGAATACGACATCACAGTAACCCCCTAGGGTGTGACTGTGTACCTGG
GATGAACATGAACAAAACCAATTGCAATTGCGATTCAGGACAGATTCACTGTTGCGTGG
CACCTGAATTCCAAGGTCAAGATGTTGCCAAGTGCAATTTCAGGGACATGATGAAAATTG
CTCCCTCTTAACTGCTCTGGAGGCTTCTTAACTTAAATGAGCTGGGAGCTATGT
TTCCCTTCACTGTAGAGCTACTGCAGAACCCAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAAATCCCTGACAGACAATTCTATGTCATTCTGAGGGAAACTA
GATATAATGGCTAACTCCAAAGAAGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAGTGGATGATCTTTCACAAGATAACATG
GCTCTTGAATATAAAATAAGAGATAATTCCAGGGCAATTCTAGTTTGTTGTTGCTCTGGAAAGCA
AGTTCTAAATTCTCAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCCAAAGTGCCTGAATACCATCTGATGTCAGGTATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTTATGATATTCCACCATCTATCAGAAAAAGAGTATGAAAAGATAATAC
TGTGTAATGTCAACCAACCAAGGTTGCACTGGGATTTGTTGAGGAACTTACAG
CACAAACACTTATGGCTGCTTGGAGGCCCTCTGGGATTATTGGTGTGATATGCTTATCA
GCTGCCCTCTCCAGAAATGAAACTGTTGATGGGGACACAGCTGTGAGGAATTACTACAG
AAACCAACCTTGTAGGTGAGCTTTACCTCTCTGATAAATCTGTGGAAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGCTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKMDPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYEYSTDFVNLTGLDSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSESLNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVAGINLTEIPDNALVGLENLESISFYDRL
IKVPHVALQKVUNLKFDLNKNPINKRIRRGDFSNMLHLKELGINNMPELISIDS LAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESIMLNSNALSA LYHGTIESLPNLKEISIHNSPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVFHDMMEICLPLIAPEFSPSNLNV
EAGSVYVSFHCRATAEPQPEIYIWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSVPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQE
YEKNNTTTLMACLGGLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTS LKVKA TIVGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTGATTAGTGTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCTCCATGTGTCTCCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTTCCCTGGG
GGTTTAAATGTCAACCTGTAGCAATGCAAATCTCAAGGAATACCTAGAGATCTCCCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCGTGTTGGATGAACATGCTGGCAGACCATTCCCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTACCA
TGTTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCGAGTAGAAATAAGTGGTTACTCTCCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTTTGAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA
TAAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTAACCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTTATTTTT
AATTAAAAGCAAATAAAGCTTAACCTTGAACCATGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQS FVLMILCFHSASMCPKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGGGCCTGGAGATGCAGGGTGAAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATTCTCTGCTGGTGT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCCGCCCGCTGGAGTGCTCGGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGCCAGTCCCCGAGGGCATCCCCACCGAG
ACCGCGCTGTGACCTGGAGCTGGAGCTCAACAGAGAACATCGTGAACGCCGTGGAGGCCGG
CTTCCCGCACCTGAGGAGCTGGAGCTCAACAGAGAACATCGTGAACGCCGTGGAGGCCGG
CTTCAACAACCTCTCAACCTCGGACGCTGGGTCTCGCAGCAACGCCGTGAAGCTCATC
CCGCTAGGCCTTCACTGGCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACACTCAAGTCACTGGAGTTGGCG
ACAATGACCTGGCTACATCTCACCGGCCCTCAGGCCCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCAGGGCGCTGTCCACCTGCAACGCCCT
CATCTGGCATGGGACCTCAACATCAATGCCACTGGGACTACTCTCTTCAAGGGC
TGTACCGACTCAAGGCTTGGAGATCTCCACTGGGCCACTTGGACACCATGACACCCAAAC
TGCCCTCATGGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCCTGCCCACTAGTCTATCTGGCTTCTCAACCTCTCTACAACCCATCA
GCACCATGGGCTCATGGCATGAGCTGGCTCCGGCTGGAGGATCCAGCTGGTGGGG
GGGAGCTGGGCTGGGGCTATGGCATGGCTCCGGCTCAACTACCTGCCGTGCTCAA
TGTCTGGCAACCAAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGGCAACCTGG
AGACACCTCATCTGGACTCAACCCGCTGGCCACTGCTGGCTCTGTGGGTCTTGGCG
CGGGCTGGGGCTCAACTCAACCGGCAAGCAGGCCACGTGCGCCACGCCAGTTGTCCA
GGGAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGG
CCCGCATCCGGGACGGCAAGGCCAGGGCTGGGACGGTGTGAGGAGGGCACACCGTGCAGTT
GTGTGGGGGGGGATGGCGACCCGGCCACCTCTGGCTCTGGCTCTACCCCGAAAGCACCT
GGTCTCAGGCAAGAGCAATGGGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGGCCAACCGGGGGCAACGAC
TCCATGCCGCCAACCTGCACTGGCAAGCTACTGCCCACTCAGCCCAACAA
GACCTTGGCTTCTCATCTCAACAGCGGGCGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCCTTCCCTTCGACATCAAGACCTCATCATGCCACCACTGGCTTCTCATCTCTTC
CTGGGGCTCGTCTCTCTGCTGGTGTGCTGTGTTCTGAGGCCGGGAAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCGAAAGTGGAGCAGGATCAGCTCCGCC
ACCGGCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGCCGGGGCAGGGACCCCCG
GGCGGGGGGGAGGGGCTGGTCGCCACCTGTCACTCTCAGTCTTCCACCTC
CTCCCTACCCCTCATCACACAGCTTCTTCTCCCTCCGGCTCCGCTCCCTGCTGCCCG
CAAGCCCTCACCACTGCCCTCTCACAGGACCTCAAGGCCAGACCTGGGACCCCCA
CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTAGCAACTTTCTGTAACTTGGGTTCAATAATTATGATTTT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLLAGGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCESQAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDFEASFPHLEELLENENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNTLKDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHINAINARDYSFKRLYRLKVLEISH
WPYLDTPNCYLQGLNLTSLISITHCNLTAVPYLAVRHLVLRFLNLSYNPISTIEGSMILHEL
LRLQEIQLVGGQLAVVEPYAFRGLNLYRVLNVSGNQLTTLEESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRRWRLNFNRQPTCATPEFVQGKEFKDFFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDSDMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFFDIKTLL
IATTMGFISFLGVVLFCVLVLLFLWSRGKGNTKHNIIEIYVPRKSDAGISSADAPRKENMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACCGCGTCCGACCTCGCCCCGGGCTCCGAAGCGGCTGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCGGGCGGGAAAGCGCGATGGGGGCCAGCCGCTCGCTCTGCTCTGCTCC
TGTTCGCCTGCTGGCGCCGGCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGTGAAACAGTGGTGGCTGGTGCACCGTGGTGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTAGCTGGTACCTCTACGCCCAAGGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTG
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCAGGGT
ATAAAATCTCATTACGGAAAAAGACACAGCCACCTAACTGTCACTTCTGGGAGCAAG
CCTGCAGCCCCGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGAT
ACAGGAAGATCCAATGGTAAACCTTCAGTGTCACTGTCAGCAGCTCGGTGACATTCCAGGGTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTGTGAAACCATGAATCTAAAGGGAGCTGAC
AGATCCACCTCTAACGCATTGAAGTTTTATACACACCCAACGTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCAGAACGCTGTGCTACACTGTGAGGGTGCAGGCAATCCAGTC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCTGTGAAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCTAACAAAGAGTGACAGTGGCACCTACGGTGCACAGCCACCA
CAACATGGGAGCTACAAGCCTACTACACCCCTAACATGTTAATGACCCAGTCCGGTGC
CCTCCTCCAGCACCTACCACGCCATCATGGTGGGATCGTGGTTCTATTGTCCTCTGCTG
CTCATCATGCTCATCTTCTTGGCCTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGGAAAAGGCTCGACGATGCTCCAGACGCCACAGGCCATCATCAATGCAAGAGGG
GGCAGTCAGGAGGGAGCAGACAAGAAGGAATTTCATTAGAGGGCCCTGCCACTCC
GCCCCCAAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGAGGGCCGCCCTCCGCTTGCTCCAGGCCACCCACCCCTGTACAGAAATGCTGC
TTGGGTGCGTTTGACTCGGTTGGAAATGGGGAGGGAGGGAGGGGGGGGGAGGGAGGG
TTGCCCTCAGCCCCCTTCGCTGGCTCTCTGCAATTGGGTATTATTATTGTAACAA
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGGTGAAGAAAAGC
AACAAAAAACAA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLLNVNDPSPVPSSSSTHYAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCAAAACCTTTCTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTCTGTCGCCAGCAGGATGGCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTTACCATTTTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTCGCTAACCTTATAATCGGGTTAGTTGCACTGG
AAAACAATGGCTTGCATGAAATCGTCTGGGGGTTCTGGGGCTGCAGCTGGTGAAAGG
CTGCACATCAACAACAAAGATCAAGTCTGGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTAAATTATTACAGAGATAAGACC CGGGGCTTCAGG
ACTTGAACAAGCTGGAGGTCTATTAAATGACAATCTCATCAGCACCCACCTGCAAC
GTGTTCCAGTATGCCCCATCACCCACCTCGAACCTCCGGGGTAACAGGCTGAAAAACAGCTGCC
CTATGAGGAGGCTTGGACAAATCTCTGGTATTGGAGATCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGGCAGGGTCTGCAAGGCCCCACAGACTGCAGGTTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTCTTGGAAACACCGAGTGGATTCTAGTCTCCGGGCCCCCTG
CCCGAAGAGAACCTTGTCTGGACCCCTGCCAACCTTTCAAGACAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCCAACAGGAGGTACAAGATCCAGGCAACTGGCAGAT
AAAATCAGAGAACAGCAGCGATAGCGAGGGTAGCTCCAGGAACAAACCCCTAGCTAAC
GTTTACCTGGCCCTGGGGCTGCAGCTGCCAACATCCCAGGGCTGGGTTAAAGATGAAC
TGCAACACAGGAACGTGAGCAGCTTGCTGATTGAGGCCAACGCTCTAACGTGCAAGGA
GCTTTTCTACGAGATAACAGATCCACAGCATCCAAAATCGCACTTTGTTGATTAAAGA
ACCTCATTTGGACCTCAGGTGGCTATCATGGATAGCAATTACCTGGCACAGCTGTCCGGGA
GAAATTGCGGGGCTGCAAACCTAGAGTACCTGAACGTTGAGGATCACGCTATCCAGCTA
TCCCTCGGGGACTTCAATGCCATGCCAAAATGAGGATCCCTCATCTCAACAAACCTG
CTGAGGTTCTGCTGGAGTGGCTGCTGGCTGGGGCTCGCTCTCTAAACTCAGCTGCAAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTCTGGACCACTTAACTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGTCTGCAACATTGCGACCTCAAGCTGTGGGA
GAACGCTTGGGTTGGAGTGTGAGTGGAGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTCATGCTCTCTCAATGAGGATCTGCTCTCAGCTGTACGCTAGGATCT
GCCAACGTTAACCTGCAACAGTAAAACAGCACTGGGTGGGGAGACCGGGACGCACTCC
AACTCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCCCGGACTGCTGCTGGT
GTTTGTGACCTCCCGCTTCACCGTGGCATGCTGTGTTTATCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACCTCTCCCGTCCGAGATAATTCCCTACAGACAGTGT
GACTCTCCCTACTGCCACAATGGGCTTAAACCGAGATGGGGCCCAAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAAGTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGGCACCCGGGGCTGGAGGGGCTGTACCCAAATCCCCCG
CCATCAGCTGGATGGGATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCT
GACCCCTTACTTAACTGCTCCCTGGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTGCCTCTTGCTGAGAGCCCCCTTGTGACAGAAAGCCAGCACGACCCCTGCTGGAG
AACTGACAGTGCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGGTTCTATAC
ATATATACATATACCATCTTATAGAGAGATAGATATCTATTCTCCCTGTGATTAG
CCCCGTGATGGCTCCCTGGCTACGCAAGGGATGGGAGTGGCAGTGGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTGTACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVITGDCVKKEKICSCNEIEGDLHVDCCEKKGFTSLQRFTA
PSTSQFYH
LFLHGNSLTRLPEFANFVNAVSLHMEENGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLRLIDPGAFQDINKLEVILINNDNLISTLPANVFQYVPITHLDLRQ
NRLKTLPYEEVLEQIPGIAEILLEDPNWDTCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLMNETTEQDLCPLKNRVDSLLPAPPAQEETFAPGPLPTPFKTNQEDHATPGSAPNGGT
KPGNWQIKIRPTAAIATGSSRNKPPLANSLPCPGGCSCDHIPGSLKMNCNNRNVSSILADLK
KLSNVQELFLRDNIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALQILIPGTFNAMPKLRLILNNNNLRLSLPVDVFA
GVSLSKLSLHNHYFMYLPVAGVLQDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEV
LMSDLKCETPVNFNRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHESNSY
LDTSRVSIISVLVPGLL VFVTSAPTVGMLVILRNRKRSKRRDANSASEINSLQTVC
DSSYWHNGPYNADGAHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

ATGTCGACTGGCTCCCTGTACCCGGGCCAGCTGTCTTGACCCCCAGAATAACTCAGGGC
TGACCGGGCTGGCAGGCCTCGCACACATTCTGTGCGGCCCTAAGGGAAACTGTGGC
CGCTGGGCCCGGGGGATCTTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGAGGG
AAGGGAGGGGAACCCGGTTGGGAACGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGGCTCTCGAGCGGAGATCCAAGTGGGAGCGAGCTCTGGCCGGGCGCTCAG
AGA**ATGAGGCCGGCGTTCGCCCCCTGTGCCCCCTCTGGCAGGCCCTCTGGCCGGGCGCTCAG**
CGCGAACACCCCCTGCGACCCTGTGCTGGCTGTCGGCCCTCGGGGCGCTGCTACAGCCTGC
ACCAACGCTACCATGAAAGCGCCAGGGGCCAGGGAGCTGACATCTTGAGGTGGGGCGCTC
AGCACCGTGTGCGGGGCCAGCTGCGCTGCGCTCTGGGGCAGGGCAGGG
GCCGGAGGGGCTCAAAGACCTGTGTCTGGGTGCGACTGGAGCGAGCGTTCCACT
GCACCCCTGGAGAACGAGCTTGTGCGGGTTCTCTGGCTGCTCCGACCCGGCGCTC
GAAAGCGACACCGCTGAGTGGGAGGGAGCCCCAACGCTCTGACCCGGCGAGATGCG
GGTACTCCAGGGCACCGCTGGGCTGAGCCGGCAGGGCTGAGGAGATGCGATGCCACTG
GCCGCAACGGTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGGCCGCCCCGG
GCCGCTCTAACTTGAGCTATCGGCCCTGGGAGCTGCGCCCTTCAAGCTGGACTT
TCCACCTGGGAGCGAGGTGAGTGGCTCTGGGGGACAGCTCCGATCTCAGTTACTGCA
TCGGGAGCAAATCGGCCCTGCTGGACAAACTCTGGGCGATGTGTTGTCTCCCTGGCC
GGGAGGTACCTCGTGTGCGAAATGCGCAGAGCTCTAACGCTAGAGCTGGGAG
CTTGGCTGCGAATGTGCTAGGGCTTCGAGCTGGGAAGGACGGCCCTCTTGTTGACCA
GTGGGAAGGACAGCCGACCTTGGGGGAGCCGGTGGCCACAGGGCCCGCCGCACT
GCAACCAGCCCCGTGCGCAGAGAACATGGCAATCAGGGTGCAGAGAACGCTGGGAGAG
ACCACTTGCTCTGAACAGACAATTCAAGTAACATCTTCTGAGATTCTCGATGGGAG
CACAGAGCAGGATGTCACCTTCAATGCTCCCTCAAGGCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCAAGTTAACTCAAGCTCTCTGCAACTCTCAGGCTT
CGACTCTCTCTGCGCGTGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTTGGTGTACT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGGCCCTTCCAGGCC
AGGAAGGAGTCTATGGGCCCCGGGCTGGAGGTGATCTGAGCCCTGCTTGGCTC
CAGTTCTGCACATTGCAACAAACAATGGGGTGAAGTCAGGGACTGTGATCTGCGGGAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCCCTTGGCTCTAGTGTGCA**TAGGGAAACAGGGGA**
CATGGGCACCTCTGTGAACAGTTTCTAGTGTGAACAGTGGGAGATATTCTTATGTTATTGGAGA
TTGTGTAACTGACAATTCTGAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCTTCTCTGATGATAGAGGAAGTGGAGTGCCTTGTAGGA
TGGTGTACTGGGGACCGGGTAGTGTGGGGAGAGATATTCTTATGTTATTGGAGA
TTGGAGAAGTGTGAACTTTCAAGACATTGGAAACAAATAGAACACAAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAATGTTATGTTCTAGGCTAGGAGTAT
ATTGGTTGCAATCCCAGGGAAAAAATAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGSKDLLFWVALEERRSHCTLENEPLRGFSWLSSDPGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAAALDFSPGTEVSALCRGQLPISVTCTADEIGARNDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRWTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSAAVVFIFVSTAVVVLVLTMTVGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACCGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCTTTAAAGTGCCCTGCCCTGCAGGGCGCTATC
CCCCGGCTACCTGGGCGCCCGCGGGTGTGCGCGTGAAGAGGGAGCGCGCGGGAGCGCGA
GCGCGGTGTGAGCGCAGCGCTGCGCAGTGTGAAGCGGGGTGTGAGCGCGGTGGTGGCGGA
GGGGCGCTGTGCGGGCGCCGGCGGTGAGCGGTGTGAGCGCGGTGGCGGA
GGGGCGCGAACGCCCTGGGCGCACTCTGCTGTGCGCAGCGGTCTACGCTGCCAT**TGA**
CAGCAGTCCCCAGAGAGACCTGTTTCACATGTGGTGGCATTCTTAAGTGGAGAGTCTGGATT
TATGGCAGTGAGGTTTCTGGAGTGACCCCTCCAATAGCAAATGAAATGACTTGGAAAATCA
CAGTCCCAGAGAAAATGAGCTGTCTCAATCCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGCCATGCCAATGGCCAGCGCATGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCAGTGGCAACAAGATGATGGTCAGA
TGATTTCTGTGCAACACAGCTGGCAATGGCTCATGGCCATGTTCCGCTGCGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCTTGACAGACCTCCGCTCTTTAAC
CCCCAACTGGCAGACCGGGATTACCCGTGAGGAGTCATTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTTAAAGTGTGAGAATTGTGATGGAGGGAGATAACTACTGC
CGATATGATTATGGCTGTGTTAATGGCGGGAGTCACAGATGCTAGAAGAATTGGAAA
GTATTTGTGGTGAATAGTCACCTGCGCAATTGTCAGTGGAGAAAATGAACCTTCTTATTGAGT
TTTATCAGACTTAAGTTAACTGCAAGTGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCCTACAACAGAACAGCTGTCAACACCACATTCCGTAAACCACGGGTTAAA
ACCCACCGTGGCTTGTGTCACAAAAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTIONTGTATTAGCCGGACTGTTATCACAAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCATTCAAGCAGCGGG
CAAGAACATGAGTGGCAGGGTCACTGCTGTGCAAGCAGTGGCCTCTCCTCAGAAGAGGT
TAAATTACATTATTGGCCAAGTAGGTGAAGTGGGGAGGCAAAATCATGCCAACACAGC
TTTATCATGATGTTCAAGACCAAGAACTCAGAAGCTCTGGATGCCATTGCTTAAAGATCTATGTT
TAACAGTGAACGTGTCATTAAAGCTGTTATTCTGCCATTGCTTAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTATAAAATTACATATTCTGCAAGAGGATTCCGAAGAGATGG
GACTGGTTGACTCTTCACATGAGGAGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTCTT
TGCTGCTGTGAGAGGAGCACTATCTGATTGGAAACCTGCCACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTGCAGCCTGGAGCGTTATTTATACATCTGTAAAGGAT
ATTTAGAATTGAGTTGTGAGATGTCAAAAAAAAGATTAGAAGTCAATATTATAGT
GTTATTTGTTCACCTCAAGCCATTGGCCCTGAGCGTGTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAAATAAAATATTAAAGGAAAAAAAAAA

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAEPEPNERGDQYCGGLLDRPSGSFKTPNWPDRTDYPAGVTCVWHIV
APKNQLIELKFEKFDFVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRGTLEGN
YCSSDFVLAGTVITTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGOVQVEDGRGKIMPNSFIMMFKTKNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCCTCGCTTCTT
CCTTCTCGTGGCCTACGAGGTCCCCAGCCTGGTAAAGAATGGGCCCATGGCCCCGAAGG
GCCTAGTCCTCACCTCCCAGTGTGCTGGGCCTCAGCCTCTTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCCTCACCTCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACACCTG
CCGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCAAAAGCAGCAGGAGGGCCGGACCTCTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCTGCGGTGGTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGCAGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCCTGCTGGCC
AGTGTGGCCTTGGCTACTTGTAGGCAGAACGCAACGCCAGGCATCTGGTATGTTGGCTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCAGGACTGTGCCAG
GCCTGCCCTAGGCTGCATGGGGCAGGGCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGTAAAACACCAGGGCGGTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAAGGCATCTGTGTAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCGAGCAGATGTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTACCGCCATCTTATTGGGCTGTGGGCCATG
ACTGGCTACTGGTTGTCAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGAGATA
ATCGCGGCCACACCTGTAGGACCTCTCCACCCACGCTGCCAGAGCTGGCTGCC
TCTCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGATTAGTG
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGACTGGCAGGCTTCACAATGTTG
ATTTCAAAAGTTTCTTAAATGGTGGTGTAGAGCTTGGCCCTGCTTAGGATTAGTG
GTCTCACAGGGTGGGGCCATCACAGCTCCCTCTGCCAGCTGCTGCACTGCCAGTTCTGT
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLEFLNLPGPIWLQPSPPPQSSSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNATAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSSELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPAGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGAEACGQCGLGYFEAERNASHLVCSCAFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKA CLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCNTTEGGYRCI CAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDVLVFTAIFIGAVAAMTGYWLRSRDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGTGTGCCCCCTGGCCAGCCCCGGG
GCCGCCCTGACGGGGAGCAGCTCCCTGGCAGGCCCTGCGGAGCTGAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTGGAGGCCAGCACACACCTGCTGGTGGTCCG
CATGGAGCAGGGCTGCCGCCAACACCGAGCTGGTGCAGGCCGTGCGGCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGCTGTCCCCGCGCAGGCCGGGCG
CGGGTGACCGTCAGTGCTGCGTCCCGCAGCACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCCGTCCACGAGAGCGGCTGGAAGGCCCGTGAACGTGACCGAGGGCGTGA
ACTTCTGGCAGCAGCTGACCCGGGGGGGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGCCCCGCTGGCGTCCGGCAGGCCACAAGCTGGTCCGCTTGCCCTGCAAGGGGC
GCCAGCCGGGCTGGGAGGCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCAGCTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGCCGAGAACCTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCGGAGCCCTGGAGGCCCTGGCTTCAAGTGGC
CGTTTCTGGGCCTCGACAGTGCATCGCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAAGGCCAGGTGGTCAGGCTGCCAACATGAGGGTGCAGAA
GTGCACTGTCGCTCGGATGGTGCCTCGCAAGGAGGCTCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGAGGGTACCGAGAGCTG
GCGATGACTGAACCTGCTGATGACAAATGCTCTGCTCTAGTGAAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGCTTCTCAGGAATGAGAACCTTGGCAACTGG
GAGCCCTTGCTCAGTTTCTCTATTCTTATTACTGCACTATATTCTAACGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCAATTGTTACTTGTCTGTCAC
TGGATCTGGGCTAAAGCTCCACCACACTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFFDVTAEVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDI GDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCCGTGTTGTGTCAGTGGCCTGATCGC**GATGGGACAAA**
GGCGCAAGTCGAGAGGAAACTGTTGTGCCCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAAATACTCT
GTGAAGTTGCTGTGCCACTCGGGCTTTCTCCCCGTGTGGAGTGGAGTGGAGTGGAGTGG
AGGAGACACCACCAAGACTCGTTGTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTGTAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAGGTCATCGT
GCTTGTGCCCTCATCCAAGCCTACAGTTAACATCCCCTCTGCCACATTGGGAGCGGG
CAGTGCAGATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACTGGTCAAAGAT
GGGATAGTGTGCTCACGAATCCAAAAGCACCGTGCCTCAGCAACTCTTCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGCTTGTACCTCTGTCAGGTCAGGAGATAACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCCATGGAGCT
GTGGAGCGGAATGTGGGGTATCGTGGCAGCGCTTGTAAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCGGTTTGCCATAGCCGAGGCCACTTGACAGAACAAAGAAAGGG
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCTGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGT**GAGCCTGGTCGGCTCACCGCTATCATCTGATTTGCCCTACT**
CAGGTGCTACCGGACTCTGGCCCTGATGTCGTAGTTCACAGGATGCCATTGTCCTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTTAATAATGTCAGCTATGTCCCC
ATCCTCCCTCATGCCCTCCCTCCCTTCTACACTGCTGAGTGGCCTGGAACCTGTTAAA
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATTTGAATAGTATCTGAGCTTGTGCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTAGAGCGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGGCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGAGTG
CCACTGGGATCCCTGCCCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGAGCTCTGTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAAGCCAAAAG
GATTAAAAACCGCTGCTCAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAGTTAGCCAGGCTGGTGGTGCATGCCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAIIILCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTGMVSEEGGN SYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFEKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGTTGGGACAGCAATGAGCCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGCGCTGGCGCTGCTGCTGCTCGGACTAGGCCT
GGAGGCCGCGAGCCGTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCCACCAAGTTCAGTCCGACCCAGTGGCTATGCCGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCTGCTAGCA
GGCGAGCTCCGTGACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCGCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTGACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCATTGGGTTATTGCAAGCTGCTGCCGTGC
TCAGTGCAAGCTGGTCACCGCCACCCCTCTCTTGTCTGGCTCCAGGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGCTGAGAACAGAACAGAC
CTCGCTGCCTGAGGACAAGCACTTGCCACCACCGTACTCAGCCCTGGCGTAGCCGGA
GGAGGAGAGCAGTGTGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAG
GGGCTGGCCCCAGGCAGCTCCAGGGGAGCTTAAGACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQCPPPGLPCCPCTGVSDCSGGTDKKL
RNCSRLA克莱尔RCTLSDDCIPLTWRCGDHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSPGNATSSSAGDQSGSPTAYGVIAAAAVALSASLVTATLL
LLSWLRAQERLRLPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCGGTCTCGCTCGTCGCGCAGCGCGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGGGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTTAGCTGGCGTGTGCTCGGCCCTGCACAGCTCACGGGGGGTT
CGATGACCTCAAGTGTGTGCTGACCCGGCATTCGGAGAATGGCTTCAAGGACCCCCAGCG
GAGGGGTTCTTGAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAGAGACTGTGTTGAAGCATTAAATGAAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTATCATCACTGTGATGAAGGATTCAAGATCCG
TACCCCGACCTACACAAATATGGTTCTTATGTCGGATGATGGAACCTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGGCTCTTCTAATGGCTATGTAACATCTGAGC
TCCAGACCTCTTCCCGTGGGACTGTGATCTCCATCGCTGCTTCCGGATTAAACCTT
GATGGGTCTCGCTATCTGAGTGTGTTACAAAACCTTATCTGGTGTGTCAGCCCACCCGGTG
CTTGCTCTGAAAGCCAAGTCTGTGACTACCTCAATGGTAGTCAAGGAGATTTCTGCT
GCCACCCCGGGCTTGTGAGCGTACAACCACGAACTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTACCAGCAGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTGGTAGACGGCGTGGCGTATGCTCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGTACATGCCCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTAGGCTCTTGAGCTGCCAA
GTCTGTATTCACTCCCAGGTGCCAAGAGAGCACCCACCTGCTCGACAACCTGTACATA
ATTGCCAGCACGGCAGAGGGAGTGGCATCACCAGCCCAGGCATCCATGCCCACTGGGT
GTTGTTCTAAGAAACTGTATTGATTAAGGAAATTCCTAAAGTGTCTGAGGTGCTCTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTCTTGTGGTTAGACAAATGAAACAA
AGCTCTGATCCCTAAATTGCTATGCTGATAGAGTGGTGAAGGCTGGAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAAAATTAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDFLEQQQQQQQPSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCDGFKLKGA
T KRLCLKHFPNGTLGWIPS
DNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLI
ITCHEGFKIRYPDLHN
MVSLCRDDGTWN
NLPI
CQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCPPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGT
VVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCI
KSEQT
WPSTTHETLTTWKIVAF
TATSVLLVLLV
ILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGP
GYMASVGQQCPLPVDDQS
PPAYPGSGD
DTGPG
GESETCDS
VSGSELLQSLYSPPRCQESTHP
ASDN
PDII
IASTAEE
VASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACACGCGTCCGCTCCGCCTCCCCCGCTCCCGTGCAGTCGGTCCGTGGCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTCGCACGCCCTGCCCGCAGCCGCTCACCCCGT
AGCGCCCGAGTGTGGGGCGCACCGAGTCGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGGGCGACGGTCGCCTGCTGAGTC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACAGAGGCCTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACATTGAGGAAGGCCAAGAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCAGATGAAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTGCATCTGATGGTACCTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAGCAATAGCACAGCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
ACAATTTAGGAACCTGGTATGTGGATGAGCCGTCTGGCAGCAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGACCCGCTGGCATGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTTCATTGCAAAATTCTGATGAGAACAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACGTCCTGAATCTGCCATAC
CTTAATCCCCAGCATTCCCCCTCTCTCCCTGTGGTACACAGTTGATGTTGGTT
GGATCTGTAGAAAAGAAAACGGGGCAGCCAGACCTAGACAAAGAACACACCAC
TGGCCCTCTCCACCAGGGAAACGCCGGACCTAGAGGTCTACAATGTCATAAGAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCTGGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCATAAGGAAATACACAGAAGGTCTATGAAACAGCTTAGATCAGTCCTGT
GGATGAGCATGGTCCCAAGACCTCTGGACCCCCACGTTGGCTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCCTCAATAATGTCACITGGTGGTTGATCTAACCTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAGATGGGCTGTGGAGCTTGGAAAACCACCTGTGTTTCCCTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATGTTTTCAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGFHWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLVL
VTTVVCVWWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDL
KNISFRVCSCGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVNEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCCCTCAGGGCGGGAGGCACAGCGGCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTTCACTGCCTTGTCGGACCCAGTGGCGCTCTGACCTCGTGGCGTACTGCCCTGCACC
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCGATGGCCAGTGTCCGGTGCACCGCAGC
CTGCTGAAGTTAAAATGGTCAGGTCGTGTTCGACACGGGGCTCGAGTCCCTCAAGCC
GCTCCCCTGGAGGAGCAGGTAGAGTGGAAACCCCAAGCTATTAGAGGTCCACCCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTCAACCAACCTCAACCCACAGGAGCTTTATTGTTCCACTAACATTTCGGAACTCG
GAGTCCACCCGGTGTGCTGGCTGGCTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGACTCTGTATCCAACTACCAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGGATGGCATTGACAGTAGTGTATAAGTGGACTTCTCATCCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCTTGACATACTGCCAACAGAACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCTAGAGAGAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCAGAACAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGATTTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTACCTTAAGCCCAGAAAAAATACCATGCACACTGCTCTCAA
ACTCAGGTGATGGAAGTGGAAATGAAGAGTACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAAATAAGTGCCTTATAACATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPLCPMLKRFARMIEQRRAVDTSLYILPKEDRESLQMAVGPFHLIES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAACTAAATTGCTGCTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCCTGCCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCAACAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGAAACAGAAAGGCCAGTGGGGCACC GTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGGTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAA GTGAA
GCACCAAGAACCGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGGAGGGCTGACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACCTTCA
GGATTGCCCTCTGGGCCTGGGGAGAACACCTGCAACC ATGATGAAGAACAGCTGGGTG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCAGT
GAGGTGCTGCACAAGGGCTATGGGCTCTGTCTGTGATGACA ACTGGGAGAAAAGGAGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGC CAGCACAGATTGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCTAATCTGTTGAGTGCCTGAATAGAA
AAAAAACACAGAAGAAGGGAGCATTACTGTCATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGGACTTAACTATTGTCGCCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACTACATCA
CCACCTTCCATGTCCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGTCCTGTTCTGAAAGAAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAAATTCTGAAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAAAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPILSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHLKGWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWFHDCTHQEDAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGTGGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCACAGGCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGCTTCGGCCCTCTTCGGCTGCTGCAGTGGTGCGCGGAAAGGCCACTCGGGAATGCTG
TGGTGGTGATCACAGGCGCACCTCAGGGCTGGGAAAGAATGTGCAAAGTCTTCTATGCT
GCGGGTGTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAACAGGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGAACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGTCTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGGA
TGTGGACAAGGGTGTGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCACATCCAGGCAAG
ATGAGCATTCCCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTCGTGCGCAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCAACCACAGCCCAGGGCGAAGCCCTGGAGGTGGCCAGGATGTTCTGCTGCTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTCTCAGCCTCATGGCCTCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGACTCTGACCAGGCCAGGGCAGAGAACGAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTCGATTTGAGACTTTAATGGAGATTTGCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAAACTAGAAAATAAAACATCTCAACAGTAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGCCAACTTGTATTGAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNA
GAGISYRG
TMDTTVDVKRV
METNYFGPVALTKALLPSMIKRRQGHIV
A
ISSI
QGKMSI
PFRSAYAASKHATQAFFDCLRA
EMEQYEIEVTVISPGYIHTNLSVNA
ITADGSRYGVMDTTT
AQGRSPVEVAQDVLA
AVGKKKD
VILADLLPSL
AVYLRTL
APGLFFSL
MASRARKER
KSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

FIGURE 58

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSVL VN NAGVV
YTSDLFLATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCGGGACCGCTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGA**TGGTGGTGCATGTGAAGGTATTG**
TTCGCTGGCTCTGTTGATGCCCTGCCCTGTGATGGGCTGTTCGCTCCCTATAACAGAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTACATTGAAGC
TGGGAAGATCAAAAAGGAAGAGAATTGAGGTTGGCTGGCCCTTCCAGGACTGAACATGA
AGAGTTATGCCGCTTCTCACCGTGATAAGACTTACAACAGCAACCTCTTCTGGTTCTCCCAGCTCAGATAACGCCAGAAGATGCCCTAGTGTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGCCATGGAACTCTTGTAAGGATGGCCCTTATGTTGTACAAGTAACATGA
CCTTGGTGCAGAGAGCTTGGACAGACAGACAGACAGCTCCATGCTTACATTGACAATCCA
GTGGGCACAGCTCAGTTACTGATGATAACCCAGGGATGCACTGAGTCATGAGGACGATG
AGCACGGGATTATAACAGTGCACTAATTCACTAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCATGGGAGCTTATGCAAGGAAATTGAGGTTGGCTGGCAACCCATTGCAACCTC
ATCCATTCCCTCAACCCCTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAGTACTTCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACACTGGTTGGCCCTTGAAGAATTACTGGATAAACTACTAGATGGCAGCTAAC
AAGTGTACCTCTTACTTCCAGAATCTACAGGATGTAATTACTATAACTTTTCTGGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGGTCACTCCAGAGGTGAGACAA
GCACATCCACGTGGGAATCAGACTTTATGATGGAAGTATAGTTGAAAAGTACTTGGGAGA
AGATAAGTACAGTCAGTTAGGCCATGGTAACTGAAATCATGATAATTATAAGGTTCTGA
TCTACAATGCCCAACTTGACATCATCTGGCAGCTGCCCTGACAGAGGCCCTTGATGGGC
ATGGACTGGAAAAGGATCCAGGAATACAAGAAGGAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGTTACATCCGGCAAGCGGGTGACTIONTCCATCAGGTAAATTATC
GAGGTGGAGGACATATTACCCATGACCAGCCTCTGAGAGCTTTGACATGATAATCGA
TTCAATTATGGAAAAGGATGGATCCTTATGTTGATTA**AACTACCTTCCAAAAGAGAACAT**
CAAGAGTTTCTATTGCTGAAAGAAAATCTGAAACAGAAAATGTCAAGGAATAAAAAAA
TTATCTTTCTATCTGCAAGATTCTCATCAATAAAATTATCCTTGAAAACAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTGGGCTTGAATAGGAAGTTTAAATTCTTAAGAGTAAGTGAAGGAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCAATAACAGAACAGTTGGCATGCCGTGAAGGT
GTGGAAATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAAGTCTAGAACAAAAGAATTCTTGAATAA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
SVPFPGLNMKSAYAGFLTVNKTYNSNLFFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLDRDFPWTTLSMLYIDNPVGTSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNV
TCGSNNYNFLRCTEPEDQLYYVFKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVP
WLETIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKKVWKIFKSDSEVAGY
TROAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWDYPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAAATCCCAGTCTGTTGGCTAACACAT
TTTCCCTTCTAACAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGTTCTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGACGGGACTCTCACTCAGGGTGAACAGCTCTG
CCTCTGTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGGGAGTGAGGTGATGAAAG
TCTAAATAGGAAGGAAATTGTGTCATAATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCCACTGGCTGGGAT
AAAGCTGCGGTAGGATAGGAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGG
TGAACTTCAACAGCCTTTAACCTCTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAGCAAGTATTAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATCTTCAACATTCTAACAGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAAGAAGGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGTC
AGGGCAGCCTTGTCTCCGGAAATTATTTGGTCTGACCACTCTGCCCTGGTGT
GCAGAATCATGTGAGGGCCAACGGGGAGGTGGAGCAGATGAGCACACAGGAGCGTCT
CCTCACCGCCGCCCTCTCACATGGAACAGAGGAGCCTGGCCCCGGGCTGGAGTGG
ACAGCGCTCTGTGTCCTGCTCATGTTCTGCTGCTGGCTGTGCTGGCCCCCAGCAGCCGC
ATGCCCTCAGTTCAGCACCTTCACTCTGGAATCTGTCAGGGACCTTCAACCACTTGCCT
CCACCAAGGGAGGGGGGCCCTATGGGGGCCATCAACGGGTCTATAAGCTGACAGGCA
ACCTGACCATCAGGTGGCTCATAACAGAGGGCAGAACAGGGACAACAAAGTCTCGTACCCG
CCCTCATGTGAGGCCCTCAGCAGTGTCAACCTCACCACAAATGTCACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCTGTCGGCTGTGGAGCCTTACACAGGGGGTCTGCA
AGCTGCTGGCTGGATGACCTTCTCATCTGGTGGAGGACATCCCACAAAGAGGAGCAACTAC
CTGTCAGTGTCAACAAGACGGGACCATGTAACGGGTGATTGTCGCTGTGAGGGTGAGGA
TGGCAAGCTCTCATGGCACGGCTGTGGATGGAGCAGGATTACTTCCCAGGCCCTGTCCA
GCCGGAGCTGGCCCGAGACCCCTGAAGTCTCAGGCGATGCTGACTATGAGCTACACAGGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCTCCACTTTGACAT
CTCTACATCTACGGCTTCTAGTGGGGCTTTCTACTTCTCACTGTCCAGGCCAGA
CCCCCTGGGGTGTGGCATCAACTCCGCTGGAGACCCCTTCTACACCTCACGGCATCTGGGG
CTCTGCAAGGATGACCCCAAGTCTCAGTACCTGTCCCTGCCCTCGGCTGCACCCGGC
CGGGGGTGGAAATACCGCCTCTGCAGGCTGTTACCTGGCCAAGCTGGGACTCACTGGCC
AGGCCTTCAATATCACAGCAGGAGCATGTAACCTTGTCCATCTCCAAAGGGCAGAAG
CACTATCACACCGCCGGATGACTCTGCCCTGTGCTCCCTATCGGCCATCAACTT
GCAGATCAAGGAGCGCTGCACTGTGCTACAGGGAGGGCAACCTGGAGCTCACTGGC
TGTGGGGAGGACGTCAGTGCAGAACAGGGCCTGTCCCCATGATGATAACTCTGTGGA
CTGGACATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCA
CAGCAGGGAGCGATGACCTCTGTGCCCTCACGTTAACACGGCTACAGCGTGGTTTG
TGGGGACTAAAGTGGCAAGCTGAAAAGGTAAGGTCTATGAGTTAGCTATTGGTGAGATTAACTATAG
ATTACCTCTCAGCAAGAGTCCCTTCTGGAGGTTAGCTATTGGTGAGATTAACTATAG
GCAACTTATTTCTGGGGAAACAAAGGTGAATGGGGAGGTAGAAGGGTTAATTGTTG
ACTTAGCTCTAGCTACTCTCCTCAGGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACCAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSDRSVVLLSVVWVLAPPAAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVKCTKAPVPIDDNCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRVYEFRCNSAITHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGCCTCCGCGCGCTGAGTGC GGATGGAGTGGGAACCCGGGCCCCCGCCTTAGAGAACACCGCATGACCA
CGTGGAGCCTCGCGCGAGGCCGCCGACGCTGGGACTCTGCTGCTGCTGCTTGGGCTTCCTGGTGTCCC
GCAGGCTGAGCTGGAGCACCCCTGTCCCTCTGGGCTCGCCACATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTCATCTGCTGGAGATTCACCTCTGGATCTGGGACTCTGGGCTTGAGCTTGAACACCCCTACACCATATGTTCCGTGGAACTCGATG
GGAGGGACCCGCTGCTGAAGATGAAGGCTGTGGCTTGAGCTTGAACACCCCTACACCATATGTTCCGTGGAACTCGATG
AGCCAGAAAAGGGCAAAATTGTGACTCTCTGGGAACCTGGGACCTGGAGCCCTGGAGCCCTTGCTCTGATGGCCGAGAGATCG
GGCTGTTGGGATTTCTGCCTCAGGCCCTACATCTGCACTGGAGATGGACCTCGGGGCTTGGCCAGCTGGTGTAC
TCGAAGACCCCTGCACTGGGCTGAGGAACACTTACAAGGGCTTACCGAACAGCTGGACCTTTATTTGACCC
TGATGTCAGGGTGTGGCCTACCTCGAGTGAAGGCTGGGGACATCTATTGCCCSTGCAAGGGATCTTGAACATG
GTTCTATAATAAAAGACCCCGCATACATGCCCTACCTCGAGAAGGACTCTGGAGACCTGGCATTTGGAACATG
TCCTGAGACAGACACAGGATGGCTGAGCAAGGGGATGTGGCCTGGAGGACTCTTGGCCACCATCAACTTGCAGT
CAACACAGAGCTGAGCTACGACCCATTCTCTTCAAGCTGGGAGGACTCAGCCCAAGATGGTGTGGAGT
ACTGGACGGGTGTTGACTCTGGGGAGGCCCTACAATATCTGGATTCTCTGGGTTTGAACACCGTGT
CTGCCATGAGGGCTCCCTACACCTTACAATGTTCAACCGGACCTGGGAGGACACACTTGGGCTTCACTGATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAAGCTGCAACAGCTTGTGACTATGATECTGTGCTGACAGAACCGGG
ATTACACGGCAAGACTACATGAAGCTTCTGGGCTCTGGGCTTCAACGGCATCCCTCTCCCTCCCCAACCTG
ACCTCTTCCCAGAGACTGGCCCTTAACGGCAGTTGACTCTGACTCTGCTGTGGAGCAGCCTCAAGTAC
TGGGGAGGCAATCTGAAGACCCATTCAATGGAGAACCTGCCAGTCAATGGGAAATGGCAAGTCT
TCGGGATCATCTCTGAAGACCCATTCACTCTGCTGGCATCTGGCATCTGGGACCTGTCATGATGGGGAGG
TGTGTTGAAACAGTATCCATAGGATCTTGGACTCTAACAGAACAGGATTTCTGTCCCCCTGATCAGGGT
ACACGGCTGAGGATCTGGGAGGATCTGGGAGGACTCTGGGAGGACTCAACTTGGGAGGAAATATTGATGACCCGCAAG
GCTTAATTGGAAATCTTCTATCTGAATGATTGCCCTCAGAAAATTCTGACATGATCTATAGGCTTGGATATGAAGAAGA
GCTCTTCTCAGAGGTTCTGGGCTGAGCAAATGGNNTTCCCTCCAGAAACACCCACATTACCTGCTTTCTCTG
TAGCTGCTTCCATCACGCTTCCACGCTTCTGGGCTTCTGGGAGGCTTCTGAAGCTGGGAGGCTGGGAGAAGGGGTTGATTCA
TCAATGGCCAGAACCTTGGAGCTTACTGGAAACATTGGACCCCAAGAGCCTTACCTCCAGGCTTCTGGTGA
GCAGGGAAATCACAGGCTCATGCTTTGGAGGAGGAGCTGGGGCTGCACTTACGGTACCGGAAACCCCC
ACCTGGGAGGAAAGCTACATTAAGTGGCGTGGGACCCCCCTCTGGCTGGGGAGGACTGGGCTC
CTCTTGGACTCTGGGCTGGCTGCTGCCACCCCTACTGCAAAGGACTCTCTTAAAGTAGCAACCTCAGGG
ACTGGGGGACTCTGGGCTGGCTGCTGCCACCCCTACTGCAAACACCTAAGGCTGCAAGGGAAAGGTGGGATGGCTCTGGG
TGGCTTGTGATGGCTTCTACAGGGCTCTGGCTGGGAGGCTTCTGGGAGGCTTCTGGGACCTCTGGGAGG
AGCTAATCAGATCGCCAGCCTTGGGCTTCAGAAAAGATGCTGAACAGTGGCCCTTGCAACGGGAGCTCACAGCC
TCGGAGCATCTGCTGACTCAGGGCTGCTTCTGCTGTTCTGGGAGGCTTCTGGGACATCTCTG
TTAATCCCGAAATCTGGGTGTGACCTGGAGGAGGGGGAGGGGGTGTCTACCTGAGCTGACTTTGTT
CTTCTTCAACACCTCTGAGCTTCTGGGATTCTGGAGGAACTGGGGCTGAGAAACAGAAATCTCACCCTGCTCTTCC
TCCCTTCCCACTCGCTGCTTCCACAGGGTGCAGGGCTGGCTGGGAGGAAACAGAAATCTCACCCTGCTCTTCC
CAAGTTGACAGTGTCTGGGTTGAGCTGAGGAGGACATGTGAGTCTTGGCAGAGGCAAGGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAACGCCATGGCCATGTCTGACATCTCC
AGGGAGGAGGACAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAACGCCATGGCCATGTCTGACATCTCCAGGG
GGAGGAGGAGGACAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAACGCCATGGCCATGTCTGACATCTCCAGGG
ACAGAAGGCCAGCTAGTGGCCCCGCTCCACCCACCCACGCCAGAACGCCAGGGCAGAGCAGGCCATTC
GAAGTGTGCTCAAGTCCGATTGAGCTTGTGCTGGGGCCAGGCCAACACCTGGCTTGGGCTACTGTCTG
GTTGCACTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLLL VVLGFL VL RRL DWST LVPL RL RQL GLQAK GWN FM LED ST FW
I FGG S I HY FRV PREY WR DR LL K MKA C GLN T LTT Y VP WNL H E PERG K FDF SG NLD LE AF VL MA
A E I GLW VIL RP GPY IC C SEMD LG GLP SW LL QDP GM RL RT TY KG FTE A VD LY FD HL MS RV VPL Q
Y KRG GP II AV QV EN EY GS Y NK D P AY MP Y V K ALE DR G IVE L L T SD N K D G L SK G I V Q G V L AT
I N L Q S T H E L Q I L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V I L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N Q S F G Y I L Y E
T S I T S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H I G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGAGGGGTGGACGGGTCAGGACC
CTGGTGAGGGTCTCTACTTGGCTTCGGGGTCAAGACGCCAGGACCTTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGGCCAGGCCCCCAGGACCTTACGCCATTCGAATGGAGAATC
CGACACGTGACGGTCTGTCGGCGTCTCAAGACTAGAGGAGCCTGTAACGCCATGGCTCC
AAGAACGCTGCTTCCGGCTTCCGGTCTGGCTGAGGGCTCAGCTGACCTACTGTCGCC
GGCACACACTCGGTGTTCTGAGTGGATAGGGGTATGACCGGTTCTCTAGACGGGCC
CGTTCGCTATGTCTGGCAGCCTGCACTACTTCTGGTACCGCGGGTCTTGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATAACAGTTTATGTGCCCTGAACTA
CCACGACCCAGCCTGGGTCTATAACTTAATGGCAGCCGGGACCTATTGCTTCTGA
ATGAGGCAGCTTAGCAGAACCTGTTGCTATACTGAGACCAAGGACCTTACATGTGAG
TGGGAGATGGGGTCTCCATCCTGGTCTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCTTACCTTCCGGCAGTGGACTCTCTGGCTCAAGGCTTCTGGCTGCCAAGATATATC
CATGGCTTATCACAAATGGGCCAACATCATTAGCATTCAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCACTGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGCTTCCACACAGATGGCCCTGAAGGACTCTAAGGTGGCTCCCG
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCTCTG
CGGAAGTATGAACCCCCTGGCCATTGGTAAACTCTGAGTACTACACAGCTGGCTGATT
CTGGGCCAGAATCACTCCACACGGTCTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAGTGGGAGCCAGTGTGAAACATGTACATGTTCCATGGAGGTACCAACTTGGATTATTGG
AATGGTGGCCGATAAGAAGGGACGCTTCCCTGGATTACTACAGCTATGACTATGTCACC
TATATCTGAAGCAGGGGACCCCACACCTAACAGCTTGTCTTGGAGATGTCACTACCAAGT
TCCAGGAAGTCTTGGACCTTACCTCCCCAGGCCAAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGGACCTTACTGGCTTCTCTAGACTTGGCTTGGCTGGGCCCAT
TCATTCAATCTGGCAATGACCTTGGGGTCAAGCAGGACCATGGCTCATGGTAC
GAACCTATATGACCCATACCAATTGGAGCCAACACCATTCTGGTGGCAAATAATGGAGTC
CATGAGCTGCTTGTGATGGTGGATGGGTCTTCAAGGGTGTGGAGGCGAAATATGAG
AGACAAATATTGGAGGGGAAACTGGGTCACACTGGGATATCTGGATATCTGGAGAACATGG
GGAGGCTCAGCTTGGGCTAACACAGTGAACCTGGCTGTTGAAGCCACCAATTCTG
GGCAAAACATCTTACCCAGTGGCAAAATGGCATATCTCAAGCTCTGGGCCACATTCT
ACTCCAAAACATTCTCAATTAGGCTCAGTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCAAGTCTGGATCAATGGGTTAACCTGGGGCGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCAAGATCTGGTTCTAGGGGAGCCCTCAACAAAATT
CAATTGCTGGAACTAGAAGATGTACCTCTCCAGGCCAACTGCAATTGGATAAGCTTAC
CTCAATAGCACTAGTACTTGCACAGGACACATCAATTCCCTTCACTGATAACCTGAG
TGCTCTGAACCAATGGAGTTAAGTGGCACTTGAAAGGTAGGCCGGCATGGTGGCTATGC
CTGTAATCCAGCATTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCACATGGTGAACCCCGTCTCCTAACAAATACAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCAGCTACTTGGGAGGCTGAGGAGGAGGAGTTGACACTG
AGGAGGAGGAGGTTGCACTGAGTGGAGGTTGACACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNHYEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFIAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGQNHSRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALARVDISKFQEVLGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMGVFQGVVERNMNRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWNWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVYPRFLFPRGAJNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCCTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCCTCACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCAGATGTCAAAAACGATTT
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATTCCAAGCGTTTGGTGTGTT
CTTGTCAAGAAGTTAGTGAAAGAAACTTACGGGAAATTAGTTGAACCATGAGTGACATTG
AAAAACTCAGGCAGCACATTCAACCAACGCCAGGACAAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGCCTGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAAGCTAAATTCTGCTAACAGATTCTCAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCAATTGAGA
TGCCTTCACGTGAAGTTCACTGTGTTGAAATTCTGCTGCTGTTGCTGATTTCTCAAAA
CCTTCGAGAGTTGACTTAATAGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACCTGAAAGAGCAATTGACCAAGTT
CCCTCCAACATTACAGATGTTGCTCACATCTAACAAAGTTAGTCATTCTAACAGGGCAC
TAAACTCTGGTACTGAAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGAACTCCAGA
ACTGTGAGCTAGAGAGAACCCCACATGCTATTTCAGCCTCTCTAACATTACAGGAACACTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAATCATCAGTTCCAGCATTAAAAGCACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACCTTATTCTCAACACAAAGCTCGAACCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTACAAACACATTCTCATGATTCCAAATAGA
AATAGGATTGCTTCAGAACCTGAGCATTGATATCAGTGGGAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCTAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAAACTG
CTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTGTTG
TGGAAGATCACCTTTTGATACCCGCCACTCGAAGTCAAAGAGGGATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCAATTAGGAGTAG
ATACATTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTCAATGTTGAGGTTTAAAGTCATTCTAACATTGTTAAATTGTTGTAACATTGGAT
GCTGCCGCTACTGAAATGTTACAAATTGCTGCCACTCGAAGTCAAAGGAGGATTGAATCAAGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEI PAWVYLLKLNRELYLIGNLNSENNKMIGLESLRELRLHKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTLKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKLNLESLYFSNNKLESLPVAVFSLQ
KLRLCDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCGGGCTTCTCTGACTTGCAATTCCATCCTTTCATGACAACAGTCTTTTATTCT
TTTTTCCATCTCTGGGCCAGCTGGGATCTAAGGGCCCTGGAAAGACATTCTGTCTTACACATAAGGAT
CTGTGTGTTGGGTTCTCTCTCCCTGCATTGGCATTGCTTACTGGTGTGTGGGGAGGGAGACACGCTGG
GCTCAGTCTTGTCTGCACTTATCTGCCATTAGGTACATCGAAAGTCTTGTGACTCCATACAGTGAATATGCCCTGTC
ATCGCTGGTGGTATCTGGCGGCCCTGCTCTGCTGATAGTTGTGCTGCTGCTTACTTCAAAATCACAAAC
GCGCTAAAAGCTGCAAGGGAAACCTGAGCTGTGGCTGAAAAAAATCACAACCCAGACAAAGGTGTGGGGCAAG
AACAGCCAGGCAAACCATGGCAACGGACTCTGTCTCCCTGCACTGTGCAAGGATATAAGATGTGCCC
AGTTTGATTCCCTGCCACCTTGTGCTGGCAATAAATGAGGGGCTGGGAGGCTCCCTCTCAA
GCAGAGGCCCTGAAGACTTCATATGATGTCATGGGCCACCTGTGTTGTGATGTGAGGCAAGAAGGCCAG
CTCCCCATCAGTTATGAAAATAACTCAGTGCCTGCTGGGAAACRGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGCAACCCCTCAGGAGAGGATGGGGAGAGAAACCTCAGTGGGAAATGCTGATAAAGGAGCTCA
CACAGCTGCTCTATTACACAAATCTACCCCTTGGCTGGCTGAACATGACGTTTCTGGAGGTGCAQAAA
GCTGATGTAACACAGGCCATAAAAGCTGCTTAAAGCTGCTTAAAGCTGCCACGCGCTTGCACAAAATGGACCTTGT
AGAAGGCTCATGCCATTGACCCCTTAAATTCTCTCTGTTGGGGAGCTGCAATGGGGAGGCTGAAAG
GCAAGCTGCACAGCTAGTCTAGGGGGTGCCTAATGGCAGAGGCCACAAAGCCATGATCTGCACTCAATCCC
AGTGAAGACTGCCACCTGCCATAAGGAAAGCAGGAAACAAACAGCAGATAATCTGAGGTTAGGGAAAGGCT
GATCAGATGGAAAGCTGTGAAAGAAAACATTAAAGTCTTGTGAGGAAACCTCCAGCAATGGGCTCTAGGG
CAAGTCTGCACTGAAACAGACTGTCTTGTCTTACTACTCTCTCTCTAACTCTCTCTCTCT
GGCGTTACCTGGATACCTGGAAAGGATCTTACAGGCCAAACGGCATCTGAGCTGGCTTAT
TGTGTGTCACCTGGAAAGGATCTTACAGGCCAAACGGCATCTGAGCTGGGAAATAGAC
AAAAGCTGCAAAATTGATTTCTGCACTTATGATGCCCTCTCAAGGCTTCTGAGGAACTCTGAGGTT
GGCCGTGTCACCTGCCACCTGATCTCAAAACTCTCTGACTGTGCTGTTCTACAGGTTATGCCAACTCT
TACCGGGGATTCTCTGCTCTCACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTGTGCTCT
GACAGGATGAGAGTTTATAAGCAATCTACCTAGAGGTTTAACCTAATGGGATAACTTGCAACTAAA
GACCCAACTTGCAGGCCAAAAATTATCAAATGTTGTGGAAATTCTGCTCCCTCTAAATGGATGTGGFACATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCTCTCAACTCTGAGTGTACCT
CGTAGGAAACAACTCCAGATTATGTGAAAGTGTGAAATGGGACATAATTCTACAGTGAGGAAATATACATAACA
GAAGATGATGTAATAACAAAGTCAAATGCACTGGCAAAATATAACACCAAGCATGGCTTTTGATCCTAA
TTGAAAAGACTATACTTGAACTACCATATTATGTTGAGTTGACCAAAACTCTTTTGTCAAGTTAGTGTG
ACCTCAGATCCAATTGGGGTTCTGATACCTGTAGAGCCCTCCACCTCTGACATTGCTACCT
TACGACCTAATCAAGAGTGTGAGTGTGAGAATGAAACTGTGAGGTTGATCTTACAGGAGCT
TCCAGTTAAATGCCCTTAAATTCTGAGAAGTGTGATCTGCTGTTCTGAGTGTGATCTG
AGCAGTGCACCACTGCTGCACTCAAGGTGTGCTCTGCCAGAACAGACATCTTCTCATATAATGG
AAAACAGATTCACATAGGACCCATTCTGCTGAAAGGGATCGAAGTGTGCAATTCTGAGTGTG
GAACACATGCCGAAGAAACTCCTAACAGCAGGCCCTTCAACAGTGTCATCTGTTCTCATGGTCTAGCTG
AATGGGTGACTGTAGCGACAATCACAGTGAGGCAATTGAAATCACAGGGCAGACTACAAATCAGGAGCTG
CAGACTTAACTAACAGGTCACCCCTAAGTGACATGTTCTCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAAATAAGGGAAGGGCTGAAAGTGCACACAGGCCCTGAGTGTAAAAAA

FIGURE 70

MELVRRLLMPLTLLILSCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYVQLDPDGSESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDPLAIYDGPSNTSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCCSDRMRVIIKSYLEAFNSNGNNIQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNITFSASSTEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIIQSQNALGKYNTSMALFESENFSFEKTILESPFYVVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFAFSPTYDLIKSGCSDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLIQCDSSDHQSRCNQGCVSRSKRDIISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFPNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGACAGCGGCCCTGC
GGACATGCGGGCCCCAGGAGCTCCCAGGCTCGCTCCCGTGTGCTGTTGCTGC
TGCTGCCGCCGCCGTCGGCTGCCCAAGCGCACCGGCTCGACCCCACCTGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCGCGCACCTCGTAGCAGTGTCTGGTGGTATTGGCAAAGGAAA
AGATACCCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTTACAGAAAATTTTTAAATGCCAACAGTGGCAGATATTTTCAAGG
CTCTGGTGCCAAATACATTGCTTAACTTCAACATCATGAGGCTTACCTTGGGGG
CAGAATATTCGGAAATCGGCATAGATGGGGCCCAAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAAGACTGACCTGCGTGGACTGACTATATTCCCTTGGCA
ATGGTTTCATCGCTCTCTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTCCAG
TTCTGAAGACATTGGCAGGAGCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTG
TCGGATGGTGCAGGGAGCACGGGATCAACTGGAAGCACAGCAGGCTTCTGGCTGGT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTGCCAAATGTATCGTGGAGCA
TCTGTAAGCATGGTGCTTTACCTGCAGTGATCTTTAAACCCAGGACATTTTG
CATAAAATGGGAAACTGCATGACAAATGCAAACTGTCTGGGCTATAGGAGGAAAGTGG
AATCTCTGCACTATCTTCAATTGAAAATGGTGAAACTTTGTAGATTTGG
GAGGAAAATTTGTGAATTTGGCCACACTAGATGGCACCATTCTGTAGTTTTGG
GCGGACTGGGAACGTGGGCTCTGGCTAAAGTGAATGGGAAGCTATTGGAACCTA
TACCTGGCGATCCCAAAATGACACTGTCCCCCAAGTGTGGTACACATCCAAGCTAAAAG
AAAAATAGTCTATGCCATTTTCTAAATGGCCCAACATGGAGACGTCTTTGGCCAT
CCAAAGCTATCTCGGGGCAAAGGAGGTAAACTATGGCCATGGACAGCCACTTACGT
GATTTCTTTGGACAAATGGCCATTTGTGACTGGCCACAGCTAACCATTCAGATGC
CGGTAAATGGCCCTGGCTTAGCCCTAAACTGTGACTAAAGTGCAGAGGTGGCT
ATGTGCAAGTTTATGTCTAAGGCTAGGAACTATCAGGTGTCTTAATGTAGCACATGG
AAGGAATGTAACTGGATAAAAATTTGGAGGTTCAGCCTTCCTTCCTTCCCATA
AATTTTTCTAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGGCCATAAAGTC
TCTTCACATGGATTTGGCTGTGTACGTCAGGGTGAGAATTTTTCCATTATTAGTAG
CAAGGAATGGGTGTTTATGGACCGGAACGTAAATTTTTGTGAAGCCATATCCCCATGT
ATTTATTAGTTTATGCATCATTAAATGTGGGAATTTTTCTGGAAATGTCATTGTCA
TTTTTTTTGTGCAAACATCATAAGGTGTTTAAAAATCCATGTGGCAATGGCTACTAC
CACCTAATGTGTATGGTAAGGTGTGTCCTAGGGTACGACAATATACAGCAGTGTAC
AAATACTGTAGGAAAATGTAACAGTGGTATTGTTAATGTAACAATATGGAAACATAGGAAG
GTACAGTAAAAAATACTGTAAAAATAAATGTGCACCTGTTAAGGGCACTACACCAGTGGAG
CTTACAGGACGTGTGAAGGTGTCTGGGTAGGTCAGTGGGTGAATGTGAAGGGCTAGGACT
TTGAACACGTGCCAAGCGTTAAATACCTGTTAGTGTCAACACTACCATTTAAAAAAA
GTTTTTTTCTTCAAATAAATAAACTAAGGTGTACTGTTAACTTAAACAGGTTTTAAA
TTTTAAACCTTTTTGGGTCTTTGTTAAAACACTTAGGTTTAAACATAAACTACTTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVPAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHWKENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATACT
TCCAGAACCTCCCATCCGGACTAGTTATTGAGCATCTGCCCTCATATCACCACTGGCCATC
TGAGGTGTTCCCTGGCTGAAAGGGTAGGCACGATGGCAGGTCTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACACAGGGCTCTGGTCCAAGGCTTTGGCTGAGAAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCCAACCGC
AGCTGAATTTCACAGAACAGCTAAGGAGGCCCTGTAGGCTGTGGGACTAAGTTGGCCGGAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGGTTGAAACTTGCAGCTATGGCTGGTTGGAGA
TGGATTCTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTG
TCCTGATTGGAAAGGTTCCAGTGAGGCCACAGTGTGAGCCTATTGTTACAACCTCATGTAT
ACTTGGACTAACCTGCAATTCCAGAACATTACACCAAAAGATCCCATTACAACACTCA
AACTGCAACACAAACAGAACATTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCCT
ACTCTACAAATACCTGCCCTACTACTACTCTCTGTCCAGCTTCCACTTCTACCG
AGAAAAAAATTGATTGTGTCACAGAACAGTTTATGGAAGATAGCACCATTGTCACAGAAC
TGAAACCATTTGGTAAATAAAGCAGCATTCAAGAACATGAAGCTGCTGGTTGGAGGTGTCC
CCACGGCTGCTAGTGCTCTCTCTTGGTGTGCACTGGTCTTGGATTTC
TATGTCAAAAGGTAATGAGGCCCTCCCTTTAACAAACAGAACATCAGCAGAACAAATGAT
CGAACACAAAGTAGTAAAGGGAGGAGAACGGCAATGATGCAACCCCTAATGAGGAATCAAAAGA
AAACTGATAAAACCCAGAACAGTCCAAGAGTCCAAGCAGAACACTACCGTGCATGCCGGAA
GCTGAAGTTAGATGAGACAGAACATGAGGAGACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCAAGCTGGGAAATCACAAAGGGCCAAAGAACCAAAGAACAGAACAG
GGTTCTAACGGTAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCAACAAAGAAC
CCTCTCCTTATTGTAACCTGTCGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCC
TTTCTAGCTGGCTATGCTCTAAATAATCCCACTGGGAGAAAGGACTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCAGTGTAAAAGGCCCTCGGTGTCAGGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTGAAAGGAGAACAGCATGCCACTGACATGTCCTCTGAGCCGGTA
AGAACAGAACATGGCAGAAAAGTTAGCCCCCTGAAAGCCATGGAGATTCTCATAAATTGAG
ACCTAATCTGTAAAGCTAAAATAAGAACATAGAACAGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAGATGTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACTACTTTCTGGTCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTAAATTTTATTTATCTGA
GTTACAGAACATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAATTGCAATAGTAGAACGCTATCTGGGAAGCTATTCTTCA
GTTTGTATTTCTAGCTTACTTCAAACACTAATTCTTATCTGAGACTAATCTT
ATTCAATTCTCTAAATATGCCAACATTATAACCTTAAATTATTATAACACATAAGAAC
TACATTGTTACCTCTATACCAAAAGCACATTAAAAGTGCCTAACAAATGTACTA
GCCCTCCTTTCCAACAGAACAGGGACTGAGAGATGCAAGAACATTGTCAGAACAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTRLLVQSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKFVSRQF
AAYCYNSSDTWNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVIALLFF
GAAAGLGFCYVKRYVKAFFPTNKNQQKEMIETKVKEEKANDSNPNEESKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCAATTGCTCTCGTGTTCGGTGCCCGACTTCACGATGG
CTCGCCCAACCTTAACCTTCTGTGCGCCCTGCTCTCTGCGCTTCACTCGTAGGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACCGAAGACGGTAACCGTGTGACTTG
ACTGGAGAGAAAGTGGAGATCTGTGATGTTCTCAGTGCCTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTCCGCTTGGATATTGCACTGGGCCTACTTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACAGAACGGGACAAGAGGGTCACTTGGATTGAGTTCTTGCCTA
TTGGTCTAATGACTGCAATCATTGGCCCTATCTATGTCGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCTGATCCTGGTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCCTCTCCTGTCATT
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTGTGTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTAAGTGCCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATTCCTCTTAG
TTGACCTGCACAGCTGGTAGACCTGATTTAACCTTAAGGTAAGATGCTGGGGTATGAA
CGCTAAGAATTCCCCAACGGACTTGTCTTCAAGCCCTCTGGCTTCGTTATGGTC
TTCATTAAGTATAAGCCTAACCTTGTGCTAGCTTAAGGAGAACCTTAACCAAAAG
TTTTTATCATTGAAGACAATTGAAACAACCCCCATTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTTAGGACTTGGAGGAGAACCTGGACTTCA
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPVRLSRWLAQPYYLALLSAAFLLVRKLPPCHGLPTQREDGNPCFDW
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTAGCCGTGAGGAGCTGCCCTGGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTCAACCTGGCATGAGGAATGGGCCTGTTGCTCCTGGTCCC
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCACTGGCAAAGACCTCTTAATGGAGTGAAAGCTGG
TGGTGGAGACACCCGAGGAGACCCGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCGGCCCTGGTCTCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTGCGAGAACGGGCCCCAGAGAAGGAGCTGGTGTGGTGGCATCGGGCTGAGGCACCGCTCT
TTGGGACTACCAAGGCCGCGTGCACCTGCCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGTGTGGCTTCCCTACAGTCCCCA
ACGGGCCGCTACAGTCACCTCCACGAGGGCCAGCAGGTCTGTGAGGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTTCCGGGCTGGAGGAGGGCCTGGACTGGTGAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCCAGCCCTGCCGTGGCC
CAGGCCGCTGCCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCTGCCAGGAAGATGATGCCAGATGCCAAGGGGGAC
AGCTTTGCCCTGGAAAGTTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTCACCCGATCTTAACGTGGGCCCCAGGCCCTGGGT
CCGAAGCTTGCTTCCCGACCCGAGAGCCGCTTGTACGGTGTACTGCTACCCGAGC
ACTAGGACTGGGCCCTCCCTGCCGATCCCTCACTGGCTGTGATTATTGAGTGGTT
CGTTTCCCTGTGGTTGGAGCATTAACTGTTTATACTCTCAATTAAATTTC
TTAACATTTTACTATTTTGTAAGCAACAGAACCCAAATGCCCTTGTCTCG
GATGCCCACTCCAGGAATCATGCTGCCCTGGCCATTGCGGTTTGCTGGCTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCTTAAGGAGGTTGGCCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGACAGTCTCCCTGCC
CAGCCTGGGGAAAGAGAGGGCTCGGGGCCCTCCGGAGCTGGCTTGGCTCTCTGCC
CACCTCTACTTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGATCTGAGGAAGGAAGAAACTCCCTCCCGTTCCCT
TCCCTCTCGGTTCAAAGAACTGTGTTGTGATTTGCTGTTCTCTGTTCCCTGTG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTGGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFVQSPNGRQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRLRHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGGATGATGTGGCGACCACATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGCCAGGGGAAGCCATCCCAGCAGCAGGCCCATGGC
CAGGGGAGGGTGCACCAGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAGCCAGGCCGCTGGGGCGGATCGTGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGCGCACACGAGCAGCGGA
CATACGGGACTGGTGAGCGCGGCCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGAGGAGCTGCGCAACGCCACCTATGGCACTACCGGCCGGTGAAGAATTTCATGAC
GTGGAGGATGAGACCTACAAAAAGATGCTGGCTGGACAGCGGGTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCTGCACCCCGAGG
AGTTCCCTCACATGGGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAAGCGAGAGGCAGCAGTCCGGACTTCCGGATCTGAAACAAGG
ATGGGCACCTGGATGGGAGTGGGTGGGCACTGGGTGCTGCCCTGCCCAGGACCGCC
CTGGTGAAGCCAACCACCTGTCACAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCTGGTAATTGAAACATGTTGTTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCGATGAGCTGTGAGCACCAGCACCTGCCACAGCCTCAGAGGCG
ACAATGACGGGAGGAGGGCCGCTGTTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCCAAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGCTGGCTTC
TGTCCCTGTCACACCCCCAACCCCAGGGAGGGCTGTCATAGTCCCAAGGATAAGCAATA
CTATTTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCTCACCACATAGACTGAAACTCCCT
GGCCCCAGCCCTCTGCTGGCTGGACACCTCCCTCTGCCAGGAGGAATA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQQKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPPEESQARLGRIVDRMDRAGDGDWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQGDMSMATE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCCGGCGGGCGGGGTGCGAGGGATCCCTGACGCCCTCTGCCCCTGTTCTTGCGCTCCAG
CCTGTCGTCGCTGTTTGCAGCCCGCCCTCCCGCGTGGCGGGGTTGACACACCAGCTTG
GGCTTCGCTCGATTGCCCGAGGGCGCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGCTGCTGTCGCTCTCCCTGCGCCGGCCGGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGGTGCAGCCGGGGCTCCCGCACCTGGCCCTGGCGCATTCTCCCTCTCTCCAG
GTGTCGAGCACCTATCAGTCAAC**AATGTC**CCGAGCCTGGATCCGGCTCGGCCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGCCCGGGCAGCAGGGAGCGCTCCATTGCTATCACATG
TTTACAGAGGGCTTGACATCAGAAAAGAAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGCTATGGCAACATAGTATATGCTCTGATTCAGCATATCTGG
GCTGCTGTCACAGGGGATAATCACCAACTCAGGGGACCTGTACGACTATACCTACC
TGGTCGAGAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTCTTCACAGTAACCTAACAGGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCACACACATCCACCAACAGCTAAAGCATAAACAGAAAACACCCAGAAGAAAATGG
CAATAAAAGATTGTAAGCAGACATTGCAATTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTAAATTACAGAAAGATTCTGGAAAGCTGCTTAATGCTTGGCTTAATGGCAACA
GAAGGACCATGTTGGGCTTGTTCAGCCAGTGAACATCCAAAATAGAATTTCAGTGA
AAACTTTACATCAGCCAAAGATGTTTGTGCAAAAGGAAGTAGGTTTCAAGGGGGTA
ATTCCAATACAGGAAAGCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGG
CTAAGGAAAGGATCCCAAAACTGGTGGTGTATTATGATGGTTGCCCTCTGATGACAT
CGAGGAAGCAGGGCATTGTGCCAGACAGATTGTTGTCATACTGATTTCAGTGA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTCAGAAGGCTGCTGT
CGGAATAATGCTTCTTCTTACACATGCCAACTGGTGGCACCACAAAATACTTAA
GCCCTGTTGACAGAGCTGCACTGTGAACAAATGATGTCAGCAAGACCTGTTAACT
CACTGAACATTGCTTCTAATTGATGGCTCAGCAGTGGAGATAAGCAATTCCGCTC
ATGCTGTAATTGTTCCAACATGCAAGACTTTGAAATCTGGACATTGGTCCAAGAT
AGCTGCTGACAGTTTACTTATGTCAGGCGCAGGGACTGAGTCACTGACTATAGCACC
AAGAGAATGTCAGTCTCATCAGAAACATCCGCTATAGTACTGGAAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGGCCCAACAAGAA
CTTCTAGTAATTGTCAGAGTGGCAGTCCCTATGATGATGTCAGGCTCTGAGCTGCTG
CACATGTCAGGAATCACTATCTCTGTTGTCAGGCTGGGACCTCTGGATGACCTG
AAAGATATGCCCTAAACCGAAGGACTCACGCTTCTACAAGAGAGTCAAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCTTGTAGAGATTCTAGAATCCAGCAAT
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTAAATTGTT
CTCATATAACTGAAATGCTTGTAGCATACTAGAAATCAGATAACAAACTATTAGTATGTCAC
AGCCATTAGGCAATAAGCACTCCCTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACACTCAGGAAAGAGGA
GATAATGTTGAGTAAACCTTAAGACTTCAACCATGCTACTAAATGTCAGATATGCAAA
TTCCATGCTCAATAAGAATCTGATACCTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCDIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFIAKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNFIIVSVAKPIPEELG
MVQDVTVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMSKTCYNSVNIACLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDFVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGACCCGGGCCCCACCGCGCCTCCGCATCTGCACCCGAGGCC
GGCGGCCCTCCCGGGGGAGCGAGCATTCAGTCGGCCCGAGCGCAACTCGGTCCAGTC
GGCGGGCGCTGGGGCGAGAGCGAGATGAGCGGCTTGGGGCACCCCTGCTGTGCGCTGC
TGCTGGCGCGGGTCCCCACGGCCCCCGCGCCCGTCCGACGGCAGCTCGGCTCAGTC
AAGCCCGGCCCCGGCTCTCAGCTACCCGAGCGAGGGAGGCCACCCCTAACATGGAGATTTCCGGGA
GGTTGAGGAACGTATGGAGGACACGAGCAGCAAAATTGCGCAGCGCTGGAAAGAGATGGAGG
CAGAAGAACTGCTGCTAAAGCATCTAGAACTGAACTTGGCAAACCTACCTCCAGCTAT
ACAATGAGAACAAACACAGACAGCAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAAAACAGACAGCAAGGACTGGAAACATGGTCTTCAAGAGACAGTTATCACATCTG
TGGGAGACCGAAAAGGAGCGAGGACAGCTGAGTCATCATCGACAGGAGACTGTGGCCCGAGC
ATGTACTGCCAGTTGCAGCTTCCAGTACACCTGCCAGGCATGCCGGGCCAGAGGATGCT
CTGCACCCGGACAGTGAAGTGTGTGGAGACAGCTGTGTGTCTGGGGTCACTGCACCCAAA
TGGCCACAGGGGCGCAACTGGGACATCTGTGACAACCCAGAGGGACTGCCAGCGGGCTG
TGTGTGCTTCCAGAGGGCTGTGTCTTCCCTGTGCAACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCCGCAGCCGGCTCTGGACCTCACCTGGAGCTAGAGCTGTG
GAGCCCTGGACCGATGCCCTGTGGGAGCTCTCTGCCAGGCCAACAGCCACAGCTG
GTGTATGTGCAAGCGACCTCTGGGGAGCGCTGACCGAGGATGGGGAGATCTGTG
CAGAGAGGTTCCCAGATGAGTATGAAGTGGCAGCTTGTGAGGAGGGTGCAGGACTGG
AGGACCTGGAGGGAGGAGCTGACTGAAGAGATGGGCTGGGGAGCTGGGCTGCCCGCT
GCACTGTCGGAGGGAGAAGAGATTAGATCTGGACCAGGTGTGGGTAGATGTGCAAGAA
ATAGCTAAATTATTCCTCCAGGTTGTGTCTTAAAGGCTGTGCAACAGGCTTCTTAC
TCTTCTCCAGTAAGTTCCCTCTGGCTGACAGCATGAGGTGTGTGCTTGTG
TCCCCCAGGGCTTCTCCAGGCTTACAGCTGTGTCTGGAGAGTCAGGCAGGGTAAAC
TGAGGGAGCAGTTGGCCACCCCTGTGCAAGGATTATGGCTGCTTGTGCTTACAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTGTATAATTGTTGAGGGAGGAGATGGAAACATGTGG
AGTCTCCCTCTGTTGGTTGGGAAATGTGGAGAAGAGTGGCCTGTGTTGCAAAACATCAA
CTCTGGGAAATATGCAAGGAAATTTCACCGAGTTCTTCCATGGGCACTAGGTAACTG
TGCTTCTCAGCTGTGCACTGGAGGAAATGTCTGTTACCCCTGCACTACATGTTTATTGATCC
AGCAGTGTGCTCAGCTCTACCTCTGTGCAAGGGCAGCATTTCTACATCCAAGATCAATT
CCTCTCTCAGCACAGCTGGGGAGGGGCTATTGTTCTCTGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGTGCTGCCAACAGCTACAGCTAGTGAAGACAGAGCAGTTCT
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCTGGTGCACCAA
AAGTGTCTCCAAAAGGAAGGAGAATGGGATTTTCTGAGGAGTGCACATCTGGAAATTAAG
GTCAAACTAATTCTCACATCCCTAAAGTAAACTACTGTAGGAAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCAATGAAGACAATGATATTGCACTGTCCCTTTGGCAGT
TGCAATTAGTAATTGAGGGCAGGATTATAATGAAATTGCAAAATCACTTAGCAGCAAC
GTACTTGTAGTAATTGAGGGCAGGATTATAATGAAATTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCACCACTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCACTGCAACTGAACTCTAGCCACTCCACAAATGATGTTTCAGGTGTC
TGGACTGTTGCCACATGATTATCCAGAGTTCTAAAGTTAAAGTTGCACTGATTGTA
TAAGCATGTTCTTGAGGTTAAATTATGATAAACATAAGTTGCACTTTAGAAATCAAGC
ATAAAACTCACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEAEAAAASSEVNLANLPPSYHNETNTDKVGNNTIHVRREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMCTRSECCG
DQLCVWGHCTKMATRGNSNGTICDNQRDCQPGLCQAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGIEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEMALGEPAAAAALLGGEET

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWAGATATVPVPPWHVCPQQCACQIRPWTWYTPRSSYREATTVDCNDFLTA
VPPALPAGTQTLQLQSNSIVRVDQSELGYLANLTTELDSQNSFSDARDCDFHALPQLLSSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFGSGLSNLLRLHILNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSLSVLAGMNIREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGKFLDLNKPLQRVGPQDFANMLHILKEGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRFHHLPQMETLMNNNALSAHQQTVESLPNLQEVLGHGNPIR
CDCVIRWANATGTRVRVFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEEPEIYWVTPAGLRITPAHAGRYYRVVPEGTIELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVVGRAALLQGRDEGGQGLELRVQETHYWILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLOVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGGCCAAGGGCGTGTGTTGAGAAGGTGAGAAGACTTCGGGACCCATTGGAGGAGGGGGACATTGTGATCCGCCT
CTCATGCGGAGAACATCATAAAGGTGATCAAGTTCATCCTCATCATCTGCTACACGGTCTACTACGTGACCAA
CATCAAGTCGACGGGACTGACCGTGACGGACATTGAGAGGCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CTCTGGGCAACACTTCAAGATCTGGCGTCTTCTACATCAGGCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CACATCTGTTGAGTGTGACTCGACGGCGCTCTCAAGAAGTACTCTGTTGAGTGTGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGCTGAAGAACAGACTTCGGCTTCATGCTGACCTTACTGACCAATAAGCAGCCGCTCTACTCCAA
GGCGTTCGGCGTCTTCTGAGGAGTGTGACTGAGAACAAAGCTGGGGCAGCTGAACTCAACAAACGAGTGGACGCT
GGACAAGCTCGGCGAGCGGCTCACAGAACAGCGCAGGGACAGCTGGAGCTGACCGCTGTTCATGCTCAGGGCAT
CCCTGACACTGTGTTGAGCTGGTGGAGGCTGACGGCTCAAGCTGGGCTCTACACACAGGGCCAAGATTGAAACGGCTGGGCT
CAGCATTGCCCAGCTCACGGGCTCACAGGGCTGTGGGCTCTACACACAGGGCCAAGATTGAAACGGCTGGGCT
GGCCATCTGGCGAGAAGCTGGGGCGTGCACATCAAGTACCTGACGGGACATCAGGGAGATCCTGGCTGTGGATCTA
TAGCTGTAGAACACTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG
CGGCTGCGGGAGGCTAACGCTCAAGGTGCTGGGCTCAAGAGCAACCTAAGCAAGCTGCCAAGGGTGGTCAC
AGAATGTTGGCGTGCACCTGGAGAACAGCTGCAATCAAACTGAGGGGCAACAGCTCATGGTCTTCAACAGCTCAA
GAAGATGGCCACCTGACTGAGCTGGAGCTGAGCTGACCTGGGCGATCTGGGCGATCCCCCCTCCATCTGGCCT
CCACAGGCTTCACTGGCTTAAGCTGTGTTGAGAACACCATGCGCTTACATCCCCATCAGAGTGGCAACCTCAACAA
CCTGGAGGCCCTCACCTGAAACGCAACAGATGGAGAAGATCCCCAACCCAGCTCTTACTGCGGCAAGCTGCG
CTAACCTGGACCTCACCAACAACTGACCTTCTGGGACCTCTGGGACCTCTGGGACCTCTGGGAGCTTCAACAGCT
AGCCATCACGGCAACCGGATCGAGCTGGCTTCCCTGGGAGCTTCTGGGAGCTTCAACAGCTGGGAGCTTCAACAGCT
GGGAAACAAACGCTGCTGACTCAGTCCCTCGGAGGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAG
CAACGGGCTGGAGTCTGGCTCTGGAGCTTCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGGGAG
GGACCTGTTCAACACACTGCCACCCGGAGGTGAAGGAGGGCTGTGGAGGGCTGACAAGGAGCAGGCCTAGCGAG
GCCGGCCAGAACAGGGACAGGACACGGCTGGGGAGGCTGGGAGCTGGGAGGCTGGGAGGCTGGGAGGAGCTGGGAG
AACTCCGGGAGAACAGGGACAGGACACGGCTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGAGCTGGGAG
GGACAGTCTGGGGGGCTTCTGGGAGCTTCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
AGCAAGTCTCAAGGGAGGAGTATTGGATAATCAGGGCTCTCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
CTGCCACAGAGGCTCTGGGACCCCTACTTCTGGGAGGCTCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
AGATAACCTATACTTCAAGGAGGAGTCACTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
CTTGGCTTATTAGGAGTCTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
CCATGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
AAGGCCAGGGCTGGAGCTTCTGGAGTCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
AAACAATTTTTTAAAAAAGCTTGGAAATGGATGGTTGGGTTTAAAAAAGAAAAAAACTTAAAAAAA
AAAAGACACTAACGGGAGCTGGAGCTGGAGCTCAGGGCAGGGTGGCAGGTTCCCTGGCAAAAGCAGGCCAGACGT
TGAACCTGTTCTCTCCCTGGGGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTTGGTCTGGAGGTT
CTTATGTTCTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
ATGTTCTCTGGGAGGACTCATTTCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
ACTCGGGTTGGCTTAATCCGGGAGTGAACGGTGTCTCATTGGCACCTCCCTCTGGCTGCCCTGGCTCTCCA
CGCACAGTCTTAAGGGAGGCAAGGGAGGCAACTTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
CCAGTGGCACCGCTGGGCTCCGCTTCCATCAGGGCTGTGGCACCTGGCTTCTCATGAAGGAGCAGACCTTA
GAGGGCTGGTGGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
CTGGAGGCTGACACACGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGGCTGGGAGG
AGAAGGGTCCCCGGCTTGGATCAATCAGTGGGAGACACTAAGGGCAAGCTTGGGAGGCTGGGAGGCTGGGAGG
CCATCGGTCTGTCGGTCTTGGTGTGCTGTCATGGGATATAATCTCAGAAATAATGACACTAG
CCTCTGACAAACATGAAGAAAAATCGTTACATGTTGAGCTGGTCAAGTGTAGACTGGTCAAGTATCRAAATRAA
ATCTATAAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLKLRQLRTKNAQDKLELHLFMLSFIGPDTVFDLVELEV
LKLELIPDVТИPPSIAQLTGLKELWLWYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVRLKSNSLSPQVVTDVGVLQKLSI
NNEGTKLIVLNSLKKMANLTELLELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEIIISFQ
HLHLRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKEKIPTQLFYCRKLRYLDSLHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVeedLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTGTGCTGCTGCCGTGCTGGGCTGAACGCAGGAGCTGTATTGACT
GGCCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGTATCTAAACCACGGAAAACCACCTGGTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCGTGGGCACTGGGTTCACTGGGTTCACTGGGTTCACTGGGTTCACTGGGTT
CTGGCTATGGGGCTTCAGACATGATGGGTTCTCTGAAGACCTTCTTCAGTTGCCAACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCGAGGGACATCAAGTGCACACTTGCGGGGT
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCTCTGGGACCTTACCTGT
ACAGCATGTCCTTCTCGAAAGACAAAGGCTGGCAGAGGTGTCTAAGGGTGCAGACAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGCTAGAATTCACACAGAGCACCTAGTTGCTTGTAGC
CACGTGAGACACCTACAACAGAGATGCCATTAGCCAGCTCATGAATGGCCCACAGAAAGAA
GCTCAAATTATTCCTGGAGGATCAATTCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGGCCAGTCATTAGCATTGTGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCCTG
GGTGCAGAAACTGAAGTGGCCAGAAGTGCCTAAATTCACTGAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCCTACAGAACCTTGCCTTC
TACTGGATTCTGAAAGCTGGTCATACTGGTCTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAUCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAAACCTAACAGATTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GТИКCNFAGVALGDSWISPVDSVLSWGPyLYSMSLLEDKGLAEVSKVAEQVLNANVKGLYRE
ATELGKAEMIIEQNTDGVNFYNIЛTKSTPTSTMESSLFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVINMEEDFMKPVISIVDELLEAGINVTVNGQLDL
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGTGCTGGCT
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCAAGTCGGCGTGGCGTGGCA
GGGGAGGCGCTGCCGTGGGATTCCCACGTATCGGGAGTCAGGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCAACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGCTCCAG
GCCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCACCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATATAAACAA
ACTCTATGTGCAACCACCTCTCTCAAGTACAGITTCGCAAGGACATCTTGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCAGGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCCACCTCTGGGCCGGTCTGAGCCTACCTGAGGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCVGVSLLSHRWLAAHCFTYSSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLsapVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVEQVIAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISSHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACAGCGTCCGGGACCGCTGGGAAGGGCAGAATGGACTCCAAGGCCGCTCCTAGGGCT
CTTGCCCCCATCCTCTGGAAATGCAGTTACAGCCGGAGCCGACCAGGGAGGACGC
TGGCCCCAGGCTGGGTGCTCTGGCCGTGCGGACCGTAGGAAAGACTGAGTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGTGCAGGCTGTGCGATCCCAG
CTCTCTCAATACGGAAAATACTGACCGCTAGAGAATCTGGCTGATCTGGTGGAGGCCATCCC
CACTGACCTCCACACGGTGAACAAATGGCTTGGCAGCGGAGGCCAGAACAGTCCATTCT
GTGATCACACAGGACTTCTGACTTGTGGCTGAGCATCGACAAGCAGAGCTGCTGCC
TGGGGCTGAGTTCATCACTATGTGGAGGACCTACGAAACCCATGTGTAAGGTCCCCAC
ATCCCTAACCGCTTACAGGCTTGGCCCCCATGTGACTTGTGGGGGGACTGCAACCGT
TTCCCCAACATCATCCCTGAGGCAACGCTTGAGCCCAAGGTGACAGGGACTGTAGGCC
GCATCTGGGGTAACCCCTGATCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACAGAACAAACAGGCAACGGCTGTGGAGCAGTATTCTGGAGCAGTATTCTCATGAC
TCAGACCTGGCTCAGTTCATGGCTCTTGGGCAACTTGTGACATCAGGATCATGAGC
CGGTGTTGGAACACAGGGCGGGCGGGCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGTGGTGCACATCTAACCTGGGCTACAGTAGGCCCTGGCCGGCATGAG
GGACAGGAGGCTTCTGAGCTGCTCATCTGCTCAGTTAGCTAGTCAGGCCCTGGCAG
GCATACTGTAGACTATGGAGATGAGGACTCCCTCAGCAGGCCATCATCCAGGGCTCA
ACACTGAGCTCATGAGGCTGCCCTCGGGGCTCACCTGCTTTCGCTCAGGTGACAGT
GGGGCGGGTTGGCTCTGGAAACGACCCAGTTCGGGCTACCTTCCCTGCTCCAG
CCCTATGTCACACAGTGGAGGACATCTCCAGGAACCTTCTCATCACAAATGAAA
TTGTTGACTATATCATGGTTGGCTTCAAGCATGTGTTCCCACGGCTTCAACAGGAG
GAAGCTGTAACGAAGTCTGAGCTCTAGCCCCACCTGCCACATCAGTTACTCATGC
CAGTGGCGCTGCCACCGAGTGGCTGCACTTCTGATGGCTACTGGGTTGGTCAACCA
GAGTGGCCATTCCATGGGTGTCGGAAACCTGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCAAG
GCTCTAACAGCAGCATGGGGCAGGGCTCTTGTGATGTAACCCGGCTGCCATGACTCTG
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGGATCCTGTAACAGGC
TGGGAACACCAACTTCCAGCTTGCT**TG**AAGACTCTACCAACCCCTGACCTTCTATC
AGGAGAGATGGCTGTCCCCCTGCCCTGAAGCTGGCAGTTGACTCCCTTATTCTGCCCTGTTG
GAAGCTGCTGAGCTGAACCTCAACTTGACTGCTGAGCACAGCTTATCTCCCTAACCTGAAA
TCTGTGAGCTTGACTTGACTCCAACCTCATGCTCATACACTCAGGTCTCCCTACT
CTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTTCAATCAGCTTTCCAAGGGTTGATACAGACTCTGTGCACTA
TTCTGATATTCACTCCCCAATTCACTGCAAGGGAGACCTCTACTGTCACCGTTACTCT
TTCTACCCCTGACATCCAGAAACATGGCTTCACTGCTGATCATCTCAATCTTGTCTTATG
GCCCTTCCATCATGGTCCCAACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACTCTCTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAAATGCTGACCTTCAATTG
TCCATTGTAGATTCTGCTTCTCATGTTACTCATGGTCCCTGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCAACTAAATAAGACTTCTATCCAATAATGATTGATACTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYKGKYLTLENVADLVRPSPLTLHTVKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNSRVPIPWVSGTSASTPVFGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEVGQGFCSGPGWDPTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCGGGCCAACCTGTCAGCGGGCAGCGAGCCGGCCGGC
GGGCTGCTCGGCAGGAACAGTCTCGGCATGGCAGGGATTCCAGGGCTCTTCCCTTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCGCATACGCCCTCTGCTGCTTGCCCCAGTCTACCCCAATTAGCCAAGCAGACT
TTGGAGCGAAGCCAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTATAAGGAACT
CCACTGCCCACTTACGAAGAGGCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAAGGGCATCTACATCCCTCAGCAGTAGTGGAGATGGGGCCAAAC
ACCGAGACTCAGGGTCTCAGGAAAAGTCTCGAAGGAAGCGGAGATTATGGCTATGACAGC
AGGTTCACTGATTGGAAAGGACTCTGCTCAACTACCCCTTCTCACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAAGCATGCTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGAACCCAGAACGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCAGGGGCCAACGACTCCACTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGACCCATGTGCCAAGGGTTGGATCAAGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGCAATTGGTGTATGCCCTCTGTGACGTCAAAGACGAGA
CCTATGACTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTGGAGCGAAAAATTATTGGATTTTCAGG
GCACCACTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTCTGGCAGCAATTAAAGGTCTCATGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCAATTGGCTGCACAGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGTATCATATCATATCATTTAACGAGTTGAAGGCATACTTTGCATAGAAAATAA
AAAAAAACTGATTTGGGCAATGAGGAATTGGACAATTAAAGTTAATCTTACGTTTG
CAAACTTGATTTTATTCATCTGAACITGTTCAAAGATTATTAATTTAGGAGAGGCC
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNIAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGDGAQHRDGSQGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPQMKFQWIRVKRTHVPKGWIKGNNANDIGMDYDYA
LLELKPKPHKRKFMKIGVSPPAKQLPGGRRIHFSGYDNDRPGNLVYRFCDVKDETYDLQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCGTCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCccccccAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCCAGCCTGTGGGAAGCCCA
GCAGCTGAACCGGGTTGGCGCGAGGACAGCACTGACAGCAGTGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACACTGCGCAGGTTCTGCTCACAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG
GGCCTGCCAGCTGGGAACCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCTGTGTATTCTGGAAGGAAGGTGCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGGCCCATCTGCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTG
CCCACCTCAGACCCCTGAGAACGCTGAAGGTCTCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGAACGGGACCCATCACTGAGGACATGCTGTGCGGGCTACTT
GGAGGGGAGCGGGATGCTTGCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGAGC
GGCGCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGCGCCTCTTAGGGCGCAGCGGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGGGGGCTCGGGGGTTTCCCCCGCTAAATAGGTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGGGAAAGGAAACCCCTCCCGACCGCCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCGCCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTATT
AGGTATTGTAAACCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWWITAHHCFKDNLNKPYLFSVLLGAWLGNPGRSQKVGA
WVEPHPVYSWKEGACADIALVRRLERSIQFSERVLPICLPPDASIHLPPTNHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCACTTGCTA
CTGCTGGTGGCACCACAGGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAAACCTCTACCGGGCCAGGTATCCCGACGGCCTCACAGCATGCTGCACATGA
GATGGGACGAGGAGCTGGCCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGGGCCAC
AACAGGAGCGGGCGCCGCGCGAGAACTCTGTCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCATGGAGGAGTGGCACCACGAGCGTGAAGCACTAACCTCAGGCCGCCACCT
GCAGCCCAGGCAGATGTGCGGCACTACACGCAGGTGTTAGGGCAAGACAGAGGGATC
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAAACATGAAATTACT
GGTGTGCAACTATGAGCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCCTCCAATGTCCCTGGCTACCACGTCAAGAACTCCCTCTGTGAACCCATCGAAGC
CCGGAAGATGCTCAGGATTGGCTTACCTGTAACGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCGCTGCTGTGGAAACCCAGGCC
CCAACCTCTTAGCACAGAAAGACCCGCCCTCATGGCAACAGAGGCTCACCTTGTAAAC
AACTGAGGTCCCTCCATTGGCAGCTCACGCTGCCCTCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCTCTAGGAGCCCAGAGAAACTCTCTGGACCCAAAGATGTCCCTGACAGGGCAAG
GGAACCTCACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTTCCAGTG
AGGTCTTGGCTCAGTTTCCAGGCCAGGACAAGGCCAGGTGAGCTGAGGCCACACTGGAC
CACACGGGGCACACCTCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTCCCTGGCTCTGCAGTCGCTTCCAGGTGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGGCCCTGGTATGTGTGGGCCCTCTCTGGGA
CTACTGCTCTGCCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTAAAGGG
TGAAGAGGTCACTGCTCTCTGTCACTCTCCCCACCCCTGCCCCAGCCCTAAACAGATA
CTTCTTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCCAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCCAACCTCTCTGCCCTCCCTCTGGCTGAGTCCTGGGGTGGAGGAGTTGAGGGAGCT
CACTGCCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCGCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATCCCTAGGGCAGATGAAGGACAAGGCCACTGGAGTGGGTTTC
TTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRMLVIELHNLYRAQVSPTASDMILHMRWDEELAAFAKAYARQCVWGHNKERGRRGLENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPGPNVKGKRPYQEGBTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPLVLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEFVTFPKSTHVPPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSCLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVSCLNSGPGHVWGPLLGLLLLPPVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETPNLGPVSAN
ITLSSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSRVTSMEP
GYFDNLANTLVLKLNRNIRSAIPFKMFKLPQLQHLELNRKIKNVNDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTETKGWLWGLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLINTLHIGNRRNSYIADCAFRLGSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRRLIQGNRIRSITKKAFTGIDALEHLDLSDNAIMSQGNNAFSQ
MKKLQQLHLNTSSLCDQCQLKWLPOWVAENNQFSFVNACAHQPLLGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMETYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMPLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAPQIAWKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTCAQN
SAGSIISANATLTVLETPSFLRPPLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTER
HFFAAGNQLLIIIVDSDVSDAGKYCTCEMSNTLGTGERGNVRLSIVPTPTCDSPQMTAPSPLDDDG
WATVGVVIIAVVCCVVGTSLVVVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAAIDLFLCPFLGSTGP
MYLKGNVYGSDFPETYHTGCPDPRTVLMHYEPSYIKKECYPCHPSEESCRSFNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDSGSEEDGKERTDFQEENHICTFKQTLENRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTNRLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEGAFNGLA
NLNTLELFDNRLTTIPNGAVFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNTLLPHDLFTPLHHLERIHLHHNPWNCNCIL
WLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSITPNGTVMTGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSIGI PGIDEVMKTTKIIIGCFVAITLMAA VMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDD EITGDTPMESHLPMPMAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCTTCRCLGDILDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIAKASSMHLQSLEVKLNNELETIPNLGPVSANIT
LISLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVILKLNRNRRISAIPPKMFKLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDFWGLSNNMEILQQLDHNNLTEITKGWLGYGLLMQELHSQAINRISPDAWEFC
QKLSELDLTPNHLRSRDDSSFLGLSLNTLHIGNNRVSYIADCAFRLGSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRLRILIQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLHLNTSSLLCDCQLKWLQPQVVAENNQFSFVNASCAPQLLKGRSIIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDPMFTA WKDNELLDAEMENYAHLRAQGGE
VMYTTTILRLREVEFASECKYQCIVSNHFQSSYSVKA KLTVNMLPSFTKTPMDLTIRAGAMA
RLECAA VGH PAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVY SCTAQNSA
GSISANATLTVLETTPSLRPLLDRVTKG TGETAVLQCIAGGS PPPKLNWT KDDSVLPVVTERHF
FAAGCNQLLIIVDSDVSDAGKYTCMSENLTGTERGNVRSLVPTPTCDSPQM TAPS LDDDGWA
TVGVVIIAVVCCVVGTSLVWWVIIYHTRRRNEDCSITNTDETNLPADIPS YLSSQGT LADRO
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD LFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKCEYPCSHPSEESCRSF SNISWP
HVRKLLNTSYSHNEGPGMKNLCLNKNSLDFS ANPASVASSNSFMGTGKALRRPHLDAYS
SFGQPSDCQPRAFYLK AHSSPDLSGSEEDGKERTDFQEENHICTFKQTL ENY RTPNFQSYLDLT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEAEQPAWFHQPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEAEEEPVVLVLSPEEPGP GPAVSCP RDACS QEGVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETINLQNNR LTSRGLPEKA FEHLTNL NYLYL ANNK
LT LAPRFLPNALISVDFAANYLTKIYGLTFGQKP NLR SVYLHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPA GLPRSLVLLHLEKNAIRSV DANV LTPIR SLEYLLLHSN
QLREQGITHPLAFQGLKRLHTVHLYNNALER VP SGLP RVR TLMILHN QITGIGREDFATTYF
LEELNLNSYNRITS PQVHRDAFRKLRLRS LDLSGNRLH TLPPGLP RVNVHVLKVKRNEAALA
RGALAGMAQLRELYLTSNR LRSRAL G PRAW VDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLK G IFLRFNKL AVGSVV DSAF RRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCCCGCAGACAGCTCGCTCCGGCCGCCGCTCCGGCTGTCTCCGGGCCAGGGCAG
CAGTAGCCGGGCCGGCGAGGGCTGGGGCTTCCTCGAGACTCTCAGAGGGGCCCTCCATCGGCCGCCCCACACC
CAACCTGTTCTCCGGGCCACTCGCTGGCCGCCAGGAGCCCTGGCCAAACTCATGATTTCCTCTGGCCCTGTG
GCTGTGATCTCTCGCTTACCTGCTGGCCGCCAGGCTTGACGAGGGTGGCCCAAGGAAATAGTGCTCATCGCC
CTGGCTATGCTGTTATGCTGGGAGGATTCAGTCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
TGTGTGCCAACACCAGTCAAACATGGTGAATGTATCGGGCCTAACACTGAGTGTCAAGGTCTCATCTGGTATTCG
AAAAACCTGTAATCAGATCTAAATGAGTGTGGCTGAGGGCCCTCTGTAAGCTGAGTGTCAAGCTGATGACACTA
CGGCAGCTACAGTGCTACTGCTCTCAACGGATATATGCTCATGCCGATGGTCTCTGCTCAAGTGCTGCCCTGACCTG
CTCCATGGCAACTCTGAGTGGCTGATGTTAAAGGCAAAATACGTTGCGAGGCTCCATCTGGCTGGCT
GACCTCTGGCTCTCATGGAGGACTCTGGTAGATGTTAGTGTCAAGGAGGCTCTGGCTGGCT
TAGGCAATGTGTCACACACTTTGGGAGCTACATCTGCAAGTGTCTATAAGGCTTCGATCTCTGATATTGGAGG
AAAATATAGGATGTCAGACAGTACAAGGAGCTACAGGGTCTGAGTGTCAAGGAGCTCTGGCTGATTTAA
CGTACTGGGCTCTACAGTCAAATGTAAGGAGGATACAGGGTCTGAGTGTCAAGGAGCTCTGGCTGATTTAA
AGTTATGATTGAACTCTCAGGCTTAACTCTGATCTAACCAAGGGAAATGGTACATTCTTAAAGGTTGCAAGGAG
TAATAATGGATTTCTGTGTTGGAAAGTCATGGTGGCTCTGGAGAACACATAATATCTCTCTATCATTACCA
CAGGCCACTCTCTAAAGCAACACAAGGACTCACCCAAGGCCAACACAAATTCTCTACTCCACCCACCCAC
CTGGCAACAGGCTCAGAACACTCTACCCAACTGAGGAGGATTACATGACAGAACAGGCTACAGACAG
ACAGCTGGCAGTACACTCTGGAGGAGGATTACATGACAGAACAGGCTACAGACAG
AGATGTTGTCAGTGTGGTACAGTGTGAAATTCTGGACATGTTGAGTGTGAGGAGAACAG
TGACTCTGGACTGGGAAACATGGGACCCAGCAGTGGCAATATGACTGACATGTCGCGCAG
GGGAAAGCTGCACGCTGGTCTACCTCTGGCCCTCATGCACTCAGGGGACTGTGCTCTGTCATCAGGCA
AGTGTGACGGGGCTGACTCTGGCAACTCTGGAGTGTGAGGAAAACACGGCTGCCAGGAGCAGCCCTGTG
GGGAGGAAATGGTGGCTCATGGTGGGAAACACAGATCATCTGGAGGCTGACATCAAGGAGGACTAC
AAGATGTAATAGGGGGTGGGAAAAGGATCTATGAGGGAAATTAAGGAAACTGGGATTATGGCAGTGTGAGG
ACTGGGAGGACTGGGCAACATTGATGGTCTTCAACTATATAAGGAGGACTGGCTTGGCAGCAGCTG
TTCTCCATATGCACTAAAGAATAGACAAGAGGAAACTGGCTTAGAGTATAAGGGAGCATTTCTGGCAGG
GGCCATTGTTGTAAGATCTTCAATAAAAAGAATGTTGAAAATCTCAGATCTCTCTCTCTTCTTAAATAATGAG
TAAAATTTGCTCTTATTAAGATGTTGAAAAGATGTTCTTCACTCCAAAGGAAAGTACAAATAATTAGAATT
AGATGTTGTTGACTCTAGTACTAGTATGCTGAGTAAATCTTCTAGAACTAAATAATTCTGAGAACGGCTTAA
CATTCCTTCTCTGACTCTTAAGGAGGAGGTTAAAGGGGAGGCCCCAACTGCTGAGCTCTACTGAAATA
TCTCTCTCTTATGGCAATCTCAGCTGATTTAAAGGAAAGGAAACTATTCTTCTTCAAAAGAGTATGATGAG
AGATATTGTTAGTACTCTAGTACTGTTCTAGTGTGGCTGGTGTGTTCTAGTGTGAAAGGTT
TTCTTCTGTTCAATGGTAGTGTGTTCTAGTGTGTTCTAGTGTGAAAGGAGGTT
ATTTCTCATGGCTGACTCTTCTCTGGTCTGTCAGGAGTGTCTTCTGCTCTGAGGAACTGGCTTGG
ACACCCGGCAGACCTTCTCTTCACTCATGATGTTGACTCTTCTTCAATTGACTCTGGCTCTTCA
AGAACAGTAATTTTGTGAACTAGTGGTACATAGAAGGCTCTCTGCTGATTTAACCTGTTAAGGAG
AGGGGGAAAATAATCAATCTGGCTTGGTAACTGGCAGGAAATATGGCTGAGTCCATTTTAA
CTCTTCTTATGGCTCTTCAATAAGCTGAGGAAAGTCTTCAAAAGGAAACTGTTAATGAGGAGG
TGATGATCTGGCTCAACTAACTGAGGAAAGGTTATCCTGGAGGAAACTGTTAATGAGGAGG
CTTAAATAAAAATGTTGTTGGTCTTCAAAATGGCTTAAATAACAAATTTCTGTTAATGAGGAGG
CTTAAATAAAAATGTTGTTGGTCTTCAAAATGGCTTAAATAACAAATTTCTGTTAATGAGGAGG
CTTAAATAAAAATGTTGTTGGTCTTCAAAATGGCTTAAATAACAAATTTCTGTTAATGAGGAGG

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNCCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GCSSSALTCSMANCQYGCVDVKGQIRCQCPSPGLHLAPDRTCVDVDECATGRASCPRFRQC
VNTEFGSYICKCHKGFDLMIYGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRTPKPTPPTPPPPLPTELRTLPLPTTPERTTGLTTIAPAASTPPGGITVDN
RVQTDPKPRGDVFSLVHSCNFHDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVAAKAPGG
KAARLVLFLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKGAHGAALWGRNGGHGWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATTGGCTCAAGGTCTTCACAACCTTCCCTTGCACAGGTGCTTCGCTGGGCGTGA
AGGTGACAGTGCCATCACACACTGTCATGGCGTCAAGGGCTCAGGGCTCACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
CACAATGCCCAAATACCTACTGGGCTCTGTGAATAAAGTCAGTCTGTTCCCTGACTTGGAAATACC
AACACAAGTTACCATGATGCCACCAATGCATCTCTGCATTACACCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGGAAATGGAACCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGTGCAGATTCTACCTCCCT
CTGGGCTGTGGAGTATGGGGAAACATGACCTGACATGCCATGTGGAAGGGGGCACTGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCCACACAGCTCACCTACTCTTTTC
TCCCCAAAACAATACCTTCATATTGCTCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGGAGGAAACCTGTCACTGAAATGGAAAGTGTATCATATTGCCCACATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGTATAAAGGGCTAAAGTAGGGGAAGTCTTACTGT
TGACCTTGGAGGAGGCCATCTATTGATTGTTCTGTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGCCTCGTTAGAAGTT
GCATCTGAGAAAGTAGGCCAGAAGACAATGGACTATGTGCTGTGCTTACAACACATAAC
CGGCAGGCAAGGATGAAACTCATTTCACTAGTATCATCACTTCCGTAGGACTGGAGAACITG
CACAGAAAGGAAAATCATTGTCACCTTCACTGAAAGTATAACTGGAATATCACTATTTTGATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAAATCATACCCCTACAAAGTTAAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTCTGTGTTCCAGATGTTCTGGTGTCCAGG
ATTCCAAGCAGGTCTGTCAGCCTCTGATTGTTGCTATGGGCAAGATTGCAAGACTACAGT
GTATGAAAGTTATTCACTGACACATCCCTGCCACAGCAGAACAGGACATCCAGAGT**TGA**ACTTTCATGG
GCTAAACAGTACATTGAGTGAIAATTCTGAAGAAACATTTTAAGGAAAACAGTGGAAAAGT
ATATTAACTGGAATCAGTGAAGAAACCCAGGACCAACACCTTACTCATTATTCTTACA
TGCAGAAATAGAGGCATTATGCAAAATTGAACTGCAGGTTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCTCACTGAGACTGCTCTCATGCTGACGG
GGAGAACGAAAGTACAGGGTTCTCATTAAGTTCTATGAAATATTCTCACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCTCACCTACAA
TGTGGAAACTTACATTGTTGCGATTTCAGCAGACATTGTTTATTAAATTTTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTTTATTCTGTTTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAGACTTGTGAACACTAAGGAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGCTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPNAPSLINPLQFPDEGNYIVKVNIQGNGLTLSAQ
KIQVTVDPPVKPVVQIHPPSGAVEYVGNMILTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMEDSIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTIYIKHGPRLLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGGAAATGGCGCCCTCCGGGAGTCTTGCAGTCCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGTCCCTGGACGCACGGGCGGGAGAACGTTCGCGTCAACGGACGAGA
ACTGGAGAGAAACTGCTGGAAAGGAGACTGGATGATAGAAATTTTATGCCCGTGGTCCCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGAAAGTAGGTAAGTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATACTGTAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCITTCAGCTATCTATGTGGA
TCAGGACGTGCATAACTACTTTATGAGACCTGGGATTCAGTGGGGATCATATACT
GTTTGTCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGATGATATTGTGGC
AGATTGCTTGTCTTCAAAAAGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT
TATTATCAGAACTGCACACACCTTTGAAAGTGGAGGAGGAACAAGAGGCGGATGGAGAA
GATGTTCAGAGAAGAGCTGAAAGTAAGAAGGAAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGGCATTCATGGCCACAGATAATCTGTTAAATTTTATAG
TTATCTTAATATTGATTTGATAAAAACAGAAGATTGATCATTTGTTGGTTGAAGTG
AACTGTACTGACTTTTGAAATTCAGGGTCACTAGTCTAGATTGCTATTAAATTGAAGAGTCTA
CATTCGAACATATAAAGCAGTACTAGTATCACAGTTGAAATATGATTAGCACAGTATGATG
GTTAAATAGTCTCTAATTGAAAATCTGCGCAAGCAATAAGATTATGATATTGT
TTAATATAAACCTATTCAAGTCTGAGTTGAAAATTACATTTCCCAAGTATTGCTATTAT
TGAGGTTATTAGAAGATTATTGAGAAAATTATTCCTCATTTGATATAATTGTTCTG
TTTCACTGTGAAAGAAAAGAGATATTCCATATAATGGGAGTTGCCCATGCTCAAG
AAATGTGATTCTAGTGACATTCGTGTTAGAGGTATATTCCAAAATTCTTGT
ATTTTAGGTATGCAACTAAAAAACACTTACATTCAATTAAATTACAGTTCTACACA
TGGTAATCAAGGATATGCTACTGATTAGGAAGTTTTAAGTTCTGATGATTCTGATT
CAACAAAGTTGATTTCTCTGATTTTCTTACTATGGGTACATTTTTATT
CAAAATTGGATGATAATTCTGGAACATTTTATGTTAGTAAACAGTATTGTTGTT
GTTTCAAACTGAGTTACTGAGAGATCCATCAAATTGACAATCTGTTGAAATTAAATT
TTGGCCACTTTTACATCATTCTGCTGAACATTCTGATTTTGCTGATGTAAGGCTTGGTA
TTTTCATTGGATGTAAGGTGAACATTCTGATTTTGCTGATGTAAGGCTTGGTA
TTTACATTGAAAGAGCTTAATAAATTACAGTTGCTCATACAGAAAGTTCTTAAATTGAT
TTACAGTCTGTAATGCTGATGTTAAAATAACATTTTATATTGTTAAAGACAA
ACTCATATTCTGTTCTCTGACTGGTAATATTGTTGAGGATTTCACAGTAAAAA
GTCAGTAGGATGGAACATTAGTGTATTCTTACTCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAATCAACATGAACTGACCTTACGTAAGAC
AATTTCTGTAATGTCCTCTTCTAGGCTGTTGCTGTAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCTCTTGAATTTAAATATTGTA
AAAGAGTTGATGTAACCTGATGCTTAGAAAATATCTAACGACACAAATAAACCT
TTCTAACCACTCATAAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFTISDKEWKSIEPVSSWFGPGSVLMSMSMALSQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GGGAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCTT
CTGTGTGCCAGAAACCGCAAGCAGTGTCAACCCAGTGGGACAGGGGATTGGAAGAGCGGG
AAGGTCTTGGCCCAGAGCAGTGTGACACTTCTGTGACCATGAAACTCTGGGTGCTGC
ATTGCTGATGGCCTGGTTGGTGTGCTGAGCTGTGTCAGGCGGAATTCTTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAAGAGAAAGAGCTGGTGCACTGAAAGACTACATC
CTTGTGGAGGAAGGCCAAGCTTCAAGATTAAGAGCTGGGCAACAAAATGGAAGGCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTCACCTGTAAATGCTCAAAACTGG
TGAAGCGCTAAACACAGACTGGCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCGCAACCTCTGTGAGCGGGCAGTTCTCCCACGTGAGGAGCAGATAGG
AGCTGCCAACGGCTGATGAGACTTCAGGACACATAACGGCTGGACCCAGGCACAAATTCCA
GAGGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGTTGGATG
GGCGCTCGGCCAACATAGAAGGGACTATTATCATACGGTGTGGATGGACAGGTGCT
AAAGCAGCTGTGAGGGGAGGAGGCCAACACAGACTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCCTCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCGCCCTGCTC
TCCCTTGACCAACAGCCAGGAACGAGCTGGAGGGATCTGGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCCAGAAGGCA
TCTATGAGGGCCCTGAGCTACCTGCCCTGAGAGGGATGTTTACGAGAGCCTCTGTGTTGG
GAGGGTGTCAAACACTGACACCCCTGAGACAGAAGAGGCTTCTGTAGGTACACCAGTGGCA
CAGGGCCCCAACAGCTCTCATGGCCCTTCAAAGAGGGAGGAGCTGGGACAGCCCGACA
TCGTCAGGACTACGATGTCATGTCAGGAGGAAATCGAGAGGATCAAGAGATCGCAAAA
CCTAAACTTGCAAGGCCACGGTCTGTGATCTTCAAGACAGGAGTCTCACTGTGCCAGCTA
CCGGGTTTCCAAAAGCTCTGGTAGAGGAAGAGTGTGACCCCTGTTGTGGCCCGAGTAAATC
GTCGGATGCCAGCATACAGGGTAAACAGTAAAGACTCAGAAATTGTTACAGGTTGCAAAAT
TATGGAGTGGGAGGACAGTATGAAACCGCATTGCACTTCTGACTTCTAGGGCACCTTTTGACAGCG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTGAGAGCTG
GTGGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCCTAAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTTCTGGGAGCCGGGAGCTGACTACCGAACAGACATGCTGCCCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCATAAGTGGTCTCATGACAGGAGACAGGAGTTCT
TGAGACCTTGTGAGTAAACAGAAGTGTGACTGACATCCCTTCTGCTCTCCCTTCTGGTC
CTTCAGCCCCATGTCACCGTGACAGACACCTTGTATGTTCTTGTATGTTCTTATCAGGCT
GATTTTTGGAGAAAATGAATGTTCTGGAGCAGAGGGAGACCATACTAGGGGACTCTGT
GTGACTGAAAGTCCCAGCCCTCATTGAGCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCTAGTGAACCAAAGTTCTGATACCTTGTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCTTACAGGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRNLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALETRRLLSLDPSHERAGGNLR
YFEQLLEEERETLTNQTEAELATPEGTYERPVDYLPERDVYESLCRGEVGVLTKTPRQKRLF
CRYHHGNRAPQQLIAPFKEEDEWDSPHIVRYYDVMSEEEIRIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQLTGLTVKAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACFVLVGCKWSNKFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCTCCTCTTTAGGAAAGACAGACCCATTCAGTGAGTGAATTTGATGT
TTCATTTAACCGTTTGGCTGGGGTAGTCTCCACACCTTCACAGTTGAAGAGCAGGAGAAGGAGTTGTGA
AGACAGGACAATCTCTGGGGATGCTGGCTGGAGGACGGCAGGGGCTTGCTCTGCTCTGCTCTGGCTCATTGACCC
CAGGTTCTCTGGTTAAACTGAAAGCTACTACTGCGCTGGGCTCAATCAATTGATCCTTGAGGCTGTGCC
CCTGGGCACCAACCTGAGGGCTTACACCATGAGCTGAGCTCCATTGAGCTGCTGCGCCAGCCTTC
CCCTCAGATTAGGCTGTCTCTGGGGTGCAGGCTGAGGCTCTGGGAGGGCACAGAATCAGATTGAGACTCTGGCTAGACAAAGTG
ATCAGAGACTCAAAACCCGGATTGTCTCCCTACTACRGAGGACCCCACAAAGCCCTACAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGGTGTCTGACCTCCGGTACTCTACTTCACCTGGGACGGGGGG
CTTGGCGCTGCTGTGACACCGTAGGGTGGCTCTGAGCCGAGCTGGCTCATGTCAGACAGACCTG
CCCGGGCTCCAGCAGGGATGAGGGTGTCTGAGCCGAGCTGGCTCATGTCAGACAGACCCATGTGCC
GCCACCTTCACACACATTGGGGCCACTACAGACTGGTCTCATGTCAGGATGACACATATGTGCC
CCCGCTGGCAGCCCTGCTGGCCACCTCAGCATCACCAAGACCTGACTTGGCCGGCAGAGGAGTCTATTG
GCCAGGGCAGACAGAGCTGGGCTTGGGACTCATGCTGGGGTCTTGGGACTTGGGACTTGGGACTTGGCT
GGCCACATCTGGATGGCTGGAGGAGACATTCTCAGTGGCCCTCTGGCTTGGACGCTGGCTCATTTG
ACTCTCTGGGGCTGGGGTGTCTCACACGACCCAGGGCAGCAGTCTGGTACCTTGAACCTGGCCAAAATAGGG
ACCCCTGAGAAAGGGAGGAGCTGGGCTTCTCTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
ACCGGCTCACAACAGCTTCAGGCTCTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
TCCGGAACTGACCGTGCACCCGAAGGGGGAGCTGAGGCTGGGCTTAAGTGAATAAGACAACTGAGGCTCAGA
CACCGACACTCTGGCTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
CTCCCCAGTGGCCACTAACGGGGTCTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
ATCAGGCTATCACCGCCGGCTGGCTTCCAGAGGCGACTCTGCAACCGGTATCGCCGCTTGGACCCAGCAC
GGGCAGTGGAGTACACCCGGGACTCTGGTGTGGAAATCTACCTATGCGCTTGGGACTTGGGACTTGGGACTTGGG
GGGTGAGGCTCTGGGGCACTGAGCCGGGGTGGAAATCTACCTATGCGCTTGGGACTTGGGACTTGGGACTTGGG
GGGTGAGGCTCTGGGGCACTGAGCCGGGGTGGAAATCTACCTATGCGCTTGGGACTTGGGACTTGGGACTTGGG
AGCTGGTCTCCACCTCTGGTGTGGAGCTGTCAGGCCCGGCTTCTCTGGAGGCTTGGAGGCTTGGGACTTGGG
TGGAGGCCAGGAAACATGCAATTGCTACCCCTGTTGGTGTGGTGTGGAGGCTGGGCAAGGAAGGTGGCCGTGGAGCTCCAG
ACCCATTCTTGGGTGAAGGCTGAGCAGCGAGGTTAGAGCAGCTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
CTGTGAGCAGAGGGCCCTTCCAGGTGCGACTCATGGAGCTGTGCTCGAAGAAGGACACCTGTGGACACTCTCT
TCTCCCTAACACCGTGTGGAAAGGCCCTGGGCCCAGACTGCTGCTCCACCGCTGTGCTGAGGCTTGGGACTTGGGACTTGGG
GGCAGGCCCTTCTTGGCTTGGAGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
CGGGGGCTGGCCCTGACCCCCCCTCCCTGTGCTGACTGACCCCTCCGGGGGGCTCTATAGGGGGGAGAATTG
ACCCGAGGCTCTGGAGGGCTGGCTTACACCTGACTACCTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
TGGCAGGCCAGGAAAGGGAGGAAAGCCCTGGAGGGGGCTGGAGGTTAGTGGATGTTTCCCTGGGTTCTCAGGGCTCC
ACCTCTTCTGGGGCGTAGAGGCCCTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGGACTTGGG
AACTCTACCCACCGCTGGCCCTCAACACTGGAGGGCTAGGGGGGGCTGGGACTTGGGACTTGGGACTTGGGACTTGGG
AGCAGGAGCAGGCCATAGACACTTACCCGGCTGGGGCCCTAACCTCATACCTTGGGACTTGGGACTTGGGACTTGGG
CCAGGAAGGGCAAGGCAAGATGGGACAGATAGAGAATTGTTGCTGATTTTTAAATATGAAATGTTATTAA
ACATGTCCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETLRHLHHTFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAAEFIGAGEQARYCHGGFGYLLRSLLLRLPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGS SAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSPVGLPAPPTPHSRFEV
LGWDYFTBQHTFSCADGAPKCP LQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFPDPARGMEYTL DLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEFAAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKA AAAAELEERRYPG
TRLAWLA VRAEAPS QVRMLDVVKSKKH PVDTLFFLTTVWTRPGPEV LNRCRMNAISGWQAFFP
VHFQE FNPALSPQRSPPGPGAGPDPPSPGADPSRGAPI GGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVM DVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGR AQLAMALF EEQE QANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAACCGTGCGCGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGGGGAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGTACTATGCTAGGACACATTAGGATTGGCATGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTC
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGAGTAAGGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACA
GTCCTCCTGACGCCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAACATGAAAAGACCTAACAGCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAAGATATCTGAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTCGAGAAAATGCAGAAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGGAGGCAATGACTTATCACCC
CAACCAAGGTAGTAGAAGGCTGTTGTCAGATGGCTGTTACTTTAAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTTGGGTATACCGCCTTAGGGCATTGGGCAATTTCAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTTGTCATTATTGTAGTAGTAACTACATATCCAA
TACAGCTGTATGTTCTTTCTTCTAAATTGGTGGCACTGGTATAACCACACATTAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTTAAACACATGAACATTGTAATG
TGGTGGAAAAGAAGTGTGTTAAGAATAATAATTGGCAAAATAACTTAAATAATATTAT
GTGATAAATTCTAATTATGAAACATTAGAAAATCTGTGGGCACATATTGGTGTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTGCTGTTCCCTTACTCTAAACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDEILKISEDERME
LSKSFRVYCIILVKPKDVSLWAATKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYLFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFNLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGTGGCCCTTCAGCAACCCCTGCACATGGCCTGAGGGGCCACCGCAGC
TCCGGCTTGCGCTCGCTGCCTGACTCTTCCTGCTGCTGCTTTCAGGGCTGCTGATAAGGGCTGTAAATC
TCAAATCGAACATCGAACCCAGCTGGTACAGGAATTGAAAGATGTGGAACACTGCTTGACATCATTCGGATTGC
AGACAGGTGACCCCCAGGTGAGGAAGAAAATTCAAGAGTAACAAACACATATGTGTTTTGACAAACAAA
TTCAAGGGAGATCTGGCGGGTGCAGAAAATACTGGGAAGACATCCTGGAAAGATCTGGAAATGTGACACGGAG
ACTCAGCCCITTATCGCTGTGAGGTCTGTGCTGAGGAATGACCCAGTGCAGCGGAAGGCTGACAGTGGCAACACTGC
CTGGCAAGTGAAGCCAGTGCACCCCTGCTGTAGAGTGCAGCGGAAGGCTGACAGTGGTATCGCAATGTGACACTGCCACGGATT
CCAGAGCCAAATCCCAAGATTTCGCAACTTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTGAGGAGCAGG
ITCAACAGGAGACTCTGGGAGTACTGACTGACTGACTGCTGACCTGGCAAGGGTGTGAGGAGCAGG
AGATGGAAAGTCTAGCCTAACATGGCGGAATTTCGGGGGGTTCTGGTTGCTCTGACTGGCCCTGA
TCACGTTGGGACATCTGGCTGTACAGACGTGGCTACTTCATCAACAAACAGGATGGAAAGTCAAGA
ACCCAGGGAAACAGATGGAGTTAACATCGCAGTACGAGGGGCCACTTCAGACACAGTCATCGTTIG
TGATCT**TGAG**ACCCGGTGTGGCTGAGGAGCAGGGCAGCTGACATACCTCTGCTAGAAACTCTGTCAA
GGCAGGGAGAGCTGACTGACTGCGACAGAGCTGACACACTTCTGCTAGAAAGCTTTCGCTTGGCAAATGTGACCA
CTACTCTTCAACTCTAACAGCCACATGAATAAGGAATTTCCTCAGGATGGACCCGGTAAATATAACACCAA
GGAGGAAACTGGGTGACTGAGTTGGTTCAATCTGTTTCTGCTAGGATGGACCCGGTAAATATAACACCAA
GTGATCTTAAAGAGTTGCTCACGTAAACGGCCGTGCTGGGCGCTGTGAGGCCAGATGGTTCACCTGGCTGTT
CAGCAGGGACACGACCACTGTGGAGGGAGGAGCAGCACAGCAGGGCATCCGGGGAAACCCA
GAAAAGGGCTTCAACAGCGCTTACTCATCGCCGGCACAGACACACCCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCGATGTCCATTGGAGGAGCTTGGGATCAGCTTGGTAAAAAACACCCAAAATCAGGAAG
GTAATTGTTGCTGGAGGGAGGATCTTCCGCTGGAGGACCTCTGCTTGTCCAACAGGGTGTGAGGATTIAAGAAA
ACCTCTGCTTAGGGCTAAGTCGAATGGTACTGAAATGTGTTTCTATGGGCTCTGTTTATTTTAAATTT
TACATCTAAATTTGGTCAAGGATTTGGTATTGAAAGAATTTCTATTTAAACTGTAAATTTAAATTT
CATACATGGTAAATTAACCTTATTGGTAAAGGTTTAAAGGTTCAACTTAAAGGTAGAGTTCAGGACTACTGTTAAAT
TGAAAATATCAATTAAGGATTGGCTTACACCAAGGGAAATCTCTGATGGAAAGTTTACTGTGATGTTCTTCT
CACACAGGTTTCTGCTTTCACAGGGAACTCATGCTGACATCTGCTTAAAGGAAACCTCTGCTTAAAGGAAACCTT
TAAAATTCAGTTAGCAATGTGAAATCAGTTGCTCATCTCTTAAAGGAAACCTCTGCTTAAAGGAAACCT
GCCTCTCTGAGGAGACTGACTGCTACCGAGGACCTGCTACGGGACACGGCCACGGGCTCAGATGTACATACAGATG
CCAGTCACTCTGGGGTTGGCCCGAGGCCCGCTAGCTGACTGCTTGTGCTGCTGGCAGGAGGCC
GCCATCTGGGCTTGGGAGTGGCTGTGCTCCAGTGGACTTACTGACTGCTGGCCCTTGCTTCACTGGACACAGC
TCTCAGGTGGGACTGGCAGGACACTGGTGTCTTCATGAGCTGGCTTCACTGGGCTCTGTAAACAGACCT
TTTGGTTATGGATGGCTACAAAATAGGGCCCGCATGCTAATTTTTTTTAAGTTTGTAAATTATT
AAGATTGCTAAAGGCAAGGAAATTCAGCTGCAAGTCTGCTAACATAACATTTTAAAGAAATGGAT
CCCATGTTCTCTTGTGCAACAGAGAACCCAGAGGCCACAGGCTCTGCTCATTCAAAACACCATGAT
GGAGTGGCTGAGCTGGCTGGCCCTTAAAGGAGCTCAGGGTGGAGCAGGCCAGGTAAAGGCCTGGGGGGAGGAAG
TGAAAAGCCTGAATCAAAAGCAGTTCTAATTGGTACTTTAATTGGTACTTCACTGGGGAGACACTGCTCATT
TGTTGGGGGACATTAGCACACATCACTCAGAAGGAGCTGTGTTCTCAAGAGGAGCTGTGAGAAGGAGC
GCCGCTGGGACTGGGACTGGACTGGAGGAGCTGAGTGTGTTCTCAGGCTTACGGCTCACATGGCCT
GCCGCTGGGACTGGACTGGAGGAGCTGAGTGTGTTCTCAGGCTTACGGCTCAGGCTTACGGCT
GAATGGCTCTACTACTCACCTGTTTCACTGGCTTCACTGGCTTCTGGTTTTTATACCTTGACAGCTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGGCCAGGGCCCTGGAGGGCA
GGAAAATGCTCCAGAGCTGGCTCAGTGTCTCCCTGGTGTCTGCTCATGCTCATCTGGAGTCTAGCATGCAAGGTC
CCTCCATATTGCAACCTTGGTAGAGGGGATGGCTCCCAACCTCAGCGTGGGGATTACGGCTCAGGCT
TCTGGTGTGCTAGTGTAGGGTAGCCATTGCCCCCTTCTTATACCTTAAACCTTCAACTAGTGTGCA
TGGGAAACAGGCTGCTAAAAGTAGAGGAGAAGTGAAGTAGAGTGTGCTGGGAAGTGTGCTTAAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTGAGGGCTGTGATTCT
GCCATTGGATGGATTTGCTGTACACAGTGTACAGACTTGTACTAACACACCGTAATTGGCTTAAAC
CTCATTTAAAGCTCAAAAAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVALITALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267